Score over length sevel 18413

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## Scientific and Technical Information Center

## SEARCH REQUEST FORM

	Requester's Full Name: TANE ZARA Examiner #: 77512 Date: 4/4/06
	Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/643,038
, ,	Location (Bldg/Room#): 3028 (Mailbox #): 2018 Results Format Preferred (circle): PAPER DISK ************************************
لع	Les home los and quality search, please attach a copy of the cover sheet, claims, and abstract or flowing 18658
24	Title of Invention: AS moder of h. PLA, groupITA
	Inventors (please provide full names): Bennett etal
	Earliest Priority Date: 5 - 25 - 01
	Search Topic:  Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the
	elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.
	*For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.
	Please Search Seg ID No: 17
	994-1070 only.
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## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%, length 8-50 nt

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.7  pyright (c) 1993 - 2006 Biocceleration Ltd.  search, using sw model  1 19, 2006, 16:13:31; Search time 0.001 Seconds (without alignments) 334.488 Million cell updates/ 0-643-038-17_994-1070  aacaagacggcctggggagaagctgatgtcctgtcaag 77	IDENTITY NUC Gapop 10.0. Gapext 0.5 119 seqs, 2172 residues hits satisfying chosen parameters: 238 length: 0	2000000000 m Match 08 m Match 1008 ig first 119 summaries	<pre>n:* nber of results predicted by chance to have a pr equal to the score of the result being print nalysis of the total score distribution. SUMMARIES</pre>	DB ID  1 US-10-956-157-18260 Sequence 1821 1 US-10-956-157-18260 Sequence 1634 1 US-10-956-157-169708 Sequence 1634 1 US-10-956-157-169708 Sequence 1634 1 US-10-956-157-150028 Sequence 1701 1 US-10-956-157-170149 Sequence 1701 1 US-10-956-157-170149 Sequence 1701 1 US-10-956-157-170149 Sequence 1701 1 US-10-956-157-16008 Sequence 1701 1 US-10-956-157-16008 Sequence 1701 1 US-09-865-866-20 Sequence 1701 1 US-09-865-866-21 Sequence 224, 1 US-09-865-866-21 Sequence 224, 1 US-09-865-866-22 Sequence 224, 1 US-09-865-866-23 Sequence 224, 1 US-09-865-866-24 Sequence 224, 1 US-09-865-866-25 Sequence 224, 1 US-09-865-866-25 Sequence 224, 1 US-09-865-866-25 Sequence 224, 1 US-09-865-866-25 Sequence 224, 1 US-10-643-038-21 Sequence 224, 1 US-10-643-038-21 Sequence 224, 1 US-10-643-038-22 Sequence 224, 1 US-10-643-038-22 Sequence 224, 1 US-10-643-038-24 Sequence 224, 1 US-10-643-038-25 Sequence 589, 1 US-10-847-918-5566 Sequence 586, 1 US-10-1719-900-154278 Sequence 586, 1 US-10-1719-900-154278 Sequence 586, 1 US-10-1719-900-154278 Sequence 586, 1 US-10-847-918-5566 Sequence 556, 1 US-10-847-918-5566 Sequence 556, 1 US-10-847-918-5566 Sequence 556, 1 US-10-847-918-5568 Sequence 556, 1 US-10-847-918-
GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd.  nucleic search, using sw model  April 19, 2006, 16:13:31 ; Search time 0.001 Seconds (without alignments) 334.488 Million cell updates/ US-10-643-038-17_994-1070 e: 77	Die: IDENTITY NUC Gapop 10.0, Gapext 0.5 119 segs, 2172 residues er of hits satisfying chosen parameters: 238	Match 08 Match 1008 First 119 summaries	uindb:* number of results predicted by chance to have a lan or equal to the score of the result being print by analysis of the total score distribution. SUMMARIES	Length DB ID  25 1 US-10-956-157-16270 25 1 US-10-956-157-162708 25 1 US-10-956-157-150028 25 1 US-10-956-157-150028 25 1 US-10-956-157-150028 25 1 US-10-956-157-150028 25 1 US-10-956-157-160028 26 US-10-956-157-160028 27 US-10-956-157-160028 28 US-10-956-157-160028 29 US-10-956-157-160028 20 US-10-956-157-160028 20 US-10-956-157-160028 20 US-10-956-157-160028 20 US-10-956-15285 20 US-10-643-038-22 20 US-10-956-153282 20 U

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APPLICANT: Wyeth
APPLICANT: Would: William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLBIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031895-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-110-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 169708
LENGTH: 25
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; Sequence 94739, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Myeth
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug; TITLE OF INVENTION: Target Genes
; TITLE OF INVENTION: Target Genes
; TITLE OF INVENTION: Target Genes
; FILLE REFRENCE: AMIJO1083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060, 756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SEQ ID NO 94739
; LENGTH: 25
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US-11-060-756-94763
US-11-060-756-94763
Sequence 94763, Application US/11060756
Publication No. UG20050221354A1
GENERAL INFORMATION:
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF PRICENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT PILING DATE: 2005-02-18
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3;
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    1 AACAAGACGGCCTGGGGATACAACT 25
                                                                                                        ; Sequence 169708, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
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                                                                                         US-10-956-157-169708
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APPLICANT: Wyeth
APPLICANT: Wounts, william
APPLICANT: Wounts, william
APPLICANT: Wounts, william
APPLICANT: Wounts,
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROFEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 18260
LENGTH: 25
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APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: 108/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 157048
LENGTH: 25
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1179, Ap
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1178, Ap
    Sequence 320928, Sequence 14594, A Sequence 181994, A Sequence 181998, Sequence 224918, Sequence 20, Appl Sequence 1178, Ap Sequence 1179, Ap
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US-10-257-017B-1320928
US-10-257-017B-14594
US-10-257-017B-181997
US-10-257-017B-181998
US-10-257-017B-181998
US-10-257-017B-224917
US-10-257-017B-224918
US-10-257-017B-224918
US-09-998-027-20
US-09-998-027-20
US-09-504-231A-1179
US-09-504-231A-1179
US-09-574-553D-1179
US-09-274-553D-1179
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100.0%; Pred. No. 5,
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US-10-956-157-157048
; Sequence 157048
; Publication No. US20050118625A1
; GENERAL INPORMATION:
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; ORGANISM: Probe Sequence
US-10-956-157-18260
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c 113
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c 114
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Sequence 141304, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TAPRILCANT: Wheth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEGARTRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEGARTRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: UNMERR: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
IENGTH: 25
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US-10-956-157-160508
US-10-956-157-160508
Sequence 160508, Application US/10956157
Sequence 160508, Application US/10956157
Sequence 160508, Application No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: 031896-043000 (AM 101081)
TITLE OF INVENTION: 2004-10-04
CURRENT PALLING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 16508
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Sequence 152285, Application US/11060756

Publication No. US20050221354A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounte, William Martin

TITLE OF INVENTION: Target Genes

FILE REFERENCE: AM101083 (031896-042000)

CURRENT APPLICATION NUMBER: US/11/060,756

CURRENT APPLICATION NUMBER: US/11/060,756

CURRENT PILING DATE: 2005-02-18

NUMBER OF SEQ ID NOS: 303284
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Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Score 21; DB 1;
100.0%; Pred. No. 9.6;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-141304
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ORGANISM: Probe Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: WILLIAM
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPERBACE: 031895-043000 (AM 100181)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARR: Patentin version 3.2
SEQ ID NO 150028
LENGTH: 25
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TITLE OF INVENTION: WOCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION WUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 170149
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                                                                                                                                                                               32.5%; Score 25; DB 1; Length 25; 100.0%; Pred. No. 3; 0; Indels tive 0; Mismatches 0; Indels
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100.0%; Pred. No. ....
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100.0%; Pred. No. ...
0; Mismatches
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Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 94763
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Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity 100.
Matches 22; Conservative
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ORGANISM: Probe Sequence
US-10-956-157-150028
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ORGANISM: Probe Sequence
US-10-956-157-170149
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Best Local Similarity
Matches 24; Conserva
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                                                                                       ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-94763
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Sequence 21, Application US/09865866

Publication No. US20030045487A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXI
TITLE OF INVENTION: ANTISENSE WOODLATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXI
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 21
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09865866

Publication No. US20030045487A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Jacquelline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXI

FILE REFERENCE: RTS-0221

CURRENT FILING DATE: 2001-05-25

CURRENT FILING DATE: 2001-05-25

SRQ ID NO 22

LENGTH: 20
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Publication No. US20030045487A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXERPLEMENT APPLICANT: US 021

FILE REFERENCE: RTS-0221

CURRENT APPLICATION NUMBER: US/09/865,866

CURRENT PILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 173

SEQ ID NO 23

LENGTH: 20
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8.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-09-865-866-22
                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-09-865-866-21
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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US-09-865-866-22/c
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US-09-865-866-19/C

1 Sequence 19, Application US/09865866

2 Publication No. US20030045487A1

3 FUBLICANT: OF THEORYTHON:

3 APPLICANT: C. Frank Bennett

4 APPLICANT: Jacquelline Wyatt

5 TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX

5 FILE REFERENCE: RTS-02.1

5 CURRENT APPLICATION NUMBER: US/09/865,866

6 CURRENT APPLICATION NUMBER: 2001-05-25

7 NUMBER OF SEQ ID NOS: 173

7 SEQ ID NO 19

7 ENGTH: 20
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| Publication No. US20030045487A1
| GENERAL INFORMATION:
| APPLICANT: C. Frank Bennet
| APPLICANT: Jacqueline Wyatt
| TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL)
| FILLE REPRESENCE: RTG-0221
| CURRENT APPLICATION NUMBER: US/09/865,866
| CURRENT PILING DATE: 2001-05-25
| NUMBER OF SEQ ID NOS: 173
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26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                    Query Match 27.3%; Score 21; DB 1; Length 25; Best Local Similarity 100.0%; Pred. No. 9.6; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                  24 AACTCTGGAGTCCTCTGAGAG 44
                                                                                                                                                                                                                                                                                   1 AACTCTGGAGTCCTCTGAGAG 21
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity
Matches 20; Conserv
                                                                 ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-152285
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US-09-865-866-20/c
                     SEQ ID NO 152285
LENGTH: 25
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LENGTH: 20
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Sequence 19, Application US/10643038
Publication No. US2005014331A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt
APPLICANTON: ANTIERNSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXIER REFERENCE: E2021
CURRENT APPLICATION NUMBER: US/10/643,038
PRIOR PLING DATE: 2003-08-18
PRIOR PLING DATE: 2001-05-25
SEQ ID NO 19
LENGTH: 20
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Publication No. US20050143331A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Uscqueline Myatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REFERENCE: RTS-021
CURRENT APPLICATION NUMBER: US/10/643,038
CURRENT FILING DATE: 2003-08-18
FRIOR APPLICATION NUMBER: US/09/865,866
FRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
FROM IN 20
FRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
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US-10-643-038-21/c
Sequence 21, Application US/10643038
Publication No. US2005014331A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wystt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REFERENCE: RTS-0221
CURRENT APPLICATION UNDBER: US/10/643,038
CURRENT PILING DATE: 2003-08-18
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Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.0%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAAACAAGACGGCCTGGGGA 20
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RESULT 18
US-10-643-038-19/c
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| Sequence 25, Application US/0865866
| Sequence 25, Application US/0865866
| Sequence 25, Application US/030045487A1
| Sequence 25, Application US/030045487A1
| Sequence 25, Application US/030045487A1
| APPLICANT: C. Frank Bennett
| APPLICANT: C. Frank Bennett
| APPLICANT: US-021
| APPLICANT: US-021
| TITLE OF INVARIANCE: RIS-022
| CURRENT APPLICATION NUMBER: US/09/865,866
| CURRENT APPLICATION NUMBER: US/09/865,866
| CURRENT FILING DATE: 2001-05-25
| NUMBER: OF SEQ ID NOS: 173
| SEQ ID NO 25
| LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REPERENCE: RTS-0221
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 24
LENGTH: 20
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                                                                                                                                        26.0%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 8.4; tive 0; Mismatches 0; Indels
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                                            FEATURE:

COTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-09-865-866-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-24
                                                                                                                                                                                                                                                                                                                                                   58 GAAGCTGATGTCCTGTCAAG 77
                                                                                                                                                                                                                                         36 CTCTGAGAGGTAAAGAGCCA 55
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  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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US-10-643-038-24/C

US-10-643-038-24/C

Sequence 24, Application US/10643038

Sequence 24, Application US/10643038

Sequence 24, Application US/10643038

Sequence 24, Application No. US20050143331A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXI

TITLE OF INVENTION: NUMBER: US/10/643,038

CURRENT PELICATION NUMBER: US/09/865,866

PRIOR FILING DATE: 2003-08-18

PRIOR FILING DATE: 2001-05-25

NUMBER: US/09/865,866

NUMBER: US/09/865,866

SEQ ID NO 24

LENGTH: 20
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Publication No. US2005014331A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTIENBER MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EXE
FILE REFERENCE: RTS-0221
CURRENT APPLICATION NUMBER: US/10/643,038
CURRENT FILING DATE: 2003-08-18
FRIOR APPLICATION NUMBER: US/09/865,866
FRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
IENGTH: 20
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      DB 1; Length 20;
8.4;
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8.4;
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8.4;
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; OTHER INFRMATION: Antisense Oligonucleotide
US-10-643-038-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Antisense Oligonucleotide US-10-643-038-24
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      ch 26.0%; Score 20; DB 1 Similarity 100.0%; Pred. No. 8.4 20; Conservative 0; Mismatches
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                                                                                             36 CTCTGAGAGGTAAAGAGCCA 55
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                                                                                                                        20 CTCTGAGAGGTAAAGAGCCA 1
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity
Matches 20; Conserv
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US-10-847-918-6072/c
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Sequence 22, Application US/10643038

Publication No. US20050143331A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REFERENCE: RTS-0221
CURRENT FAPLICATION NUMBER: US/10/643,038
CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: US/09/865,866
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 23
SEQ ID NO 23
LENGTH: 20
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Publication No. US2005014331A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennet
APPLICANT: C. Frank Bennet
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL)
FILE REFERENCE: RTS-0221
CURRENT FILING DATE: 2003-08-18
FRIOR PILING DATE: 2003-08-18
PRIOR PLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 22
LENGTH: 20
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Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                ; OTHER INFORMATION: Antisense Oligonucleotide US-10-643-038-21
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US-10-643-038-22
           PRIOR APPLICATION NUMBER: US/09/865,866
                                                                                                                                                                                                                                                                                                                                   23 CAACTCTGGAGTCCTCTGAG 42
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                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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                            PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 21
LENGTH: 20
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Best Local Similarity
Matches 20; Conserva
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US-10-643-038-23/c
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US-10-643-038-22/c
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Publication No. US20040146910A1

GRURRAL INFORMATION:

FILE REFERENCE:

FILE REFERENCE: 3527.1

FILE REPERICATION NUMBER: US/10/719,956

CURRENT APPLICATION NUMBER: 60427,836

FRIOR FILING DATE: 2003-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Sequence 154278 Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:

APPLICATH: Kue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2003-11-20

PRIOR PILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: MICTOALTAY Probe Sequence Listing Generator V 1.1

SEQ ID NO 154278

LENGTH: 25
                                                                                                                                                                                                                23.1%; Score 17.8; DB 1; Length 25; 90.5%; Pred. No. 24; tive 0; Mismatches 2; Indels
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PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 589182
LENCTH: 25
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Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches
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Pred. No. 25
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Best Local Similarity 83.3%;
Matches 20; Conservative (
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US-10-719-956-632892
                                                                                                                                                                                                                  Query Match 23.1
Best Local Similarity 90.5
Matches 19; Conservative
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                                                                                                                         ; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-589182
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                                                                  APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Be, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVEXTION: Compositions and Methods for Diagnosing and Treating Cancers
TITLE OF INVEXTION: Compositions and Methods for Diagnosing and Treating Cancers
TITLE OF INVEXTION NUMBER: US/10/847,918
CURRENT APPLICATION NUMBER: US 60/471,729
PRIOR FILING DATE: 2003-05-20
NUMBER: OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
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TILLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.1
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
FILING DATE: 2005-01-13
FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NOS: 991174
SEQ ID NOS: 991174
SEQ ID NO 81949
LENGTH: 25
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Publication No. US20050214623A1
GENERAL INPORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT PILING DATE: 2005-01-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.8;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/536,639
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US-11-036-3317-81949/c
Sequence 81949, Application US/11036317
Sequence No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
Sequence 6072, Application US/10847918
Publication No. US20050119210A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA ORGANISM: RNA1-antisense strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.1%;
Best Local Similarity 90.5%;
Matches 19; Conservative
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US-11-036-317-81949
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US-11-036-317-589182/c
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LENGTH: 21
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Weth

APPLICANT: Liu, Weth

APPLICANT: Liu, Weth

APPLICANT: Liu, Wei

TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers

TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers

TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers

CURRENT APPLICATION NUMBER: US /10/847,918

CURRENT FILING DATE: 2004-05-19

FRIOR FILING DATE: 2003-05-20

NUMBER OF SEQ ID NOS: 14937

SOFTWARE PATENTIN VERSION 3.2

SEQ ID NO 5566

LENGTH: 21
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APPLICANT: In, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Slouim, Donne
APPLICANT: Slouim, Donne
APPLICANT: Slouim, Donne
APPLICANT: Slouim, Donne
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-055000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
PRIOR PILLIAGE DATE: 2004-05-19
PRIOR PILLING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 5568
LENGTH: 21
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Pred. No. 23;
0; Mismatches 2; Indels
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; Publication No. US20050119210A1
; GENERAL INFORMATION:
Sequence 5566, Application US/10847918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AGAGCCAGCGAAGCTGATGT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 AGAGCCAGCGAAGCTGATGT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: RNAi-antisense strand
US-10-847-918-5568
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Best Local Similarity 90.0%;
Matches 18; Conservative
                       Publication No. US20050119210A1
GENERAL INFORMATION:
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Matches 18; Conservative
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US-10-847-918-5566
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Sequence 4, Application US/10422475

Sequence 4, Application WS/10422475

Publication No. US20030235813A1

GENERAL INFORMATION:
APPLICANT: LOYEN, Frank
APPLICANT: Dell'Accio, Francesco
TITLE OF INVENTION: To vivo assay and molecular markers for testing the phenotypic
TITLE OF INVENTION: autologous transplantation
TITLE OF INVENTION: autologous transplantation
FILE REFERENCE: T2420-US
CURRENT APPLICATION NUMBER: US/10/422,475

CURRENT PILING DATE: 2003-04-24

PRIOR PLLING DATE: 2002-04-24

PRIOR PLLING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

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                                                                        Sequence 338409, Application US/10719900
; Sequence 338409, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
    TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
    TITLE OF INVENTION: WIMBER: US/10/719,900
    CURRENT FILING DATE: 2003-11-20
    PRIOR APPLICATION NUMBER: 60/427,808
    PRIOR FILING DATE: 2003-11-20
    NUMBER OF SEQ ID NOS: 982914
    SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
    SEQ ID NO 338409
    LENGTH: 25
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83.3%; Pred. No. 25
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25 TAAAGAGGCAGCGAAGCTCAGCTC
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i_LOCATION: (1)...(20)
cother information: RASF-A PLA2
US-10-422-475-4
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Best Local Similarity 100.
Matches 17; Conservative
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Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Mus musculus
US-10-719-900-338409
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US-10-847-918-5566
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Sequence 5571, Application US/10847918; Publication No. US20050119210A1; GENERAL INFORMATION:
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Publication No. US20050119210A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                     68
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; ORGANISM: RNAi-antisense strand
US-10-847-918-5571
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        NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 5569
LENGTH: 21
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                                                                                                                                                                                Query Match 21.3
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-5569
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US-10-847-918-6071
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APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-0526000 (AMI01264)
CURRENT APPLICATION NUMBER: US/10/647,918
CURRENT FILING DATE: 2004-05-19
PRIOR PILING DATE: 2004-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 6070
LENGTH: 21
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APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT FILING DATE: 2004-05-19
PRIOR FILING DATE: 2005-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 5567
LENGTH: 21
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Publication No. US20050119210A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Hower Steve
APPLICANT: Liu, Wei
APPLICANT: Hower, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REPERENCE: 031896-055000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT PILING DATE: 2004-05-19
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                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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PRIOR FILING DATE: 2003-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5567, Application US/10847918; Publication No. US20050119210A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         49 AGAGCCAGCGAAGCTGATGT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-5567
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                                                                                                                                                                                                                                             ; TYPE: DNA; CORGANISM: Homo sapiens
US-10-847-918-6070
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Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 14; Conserv
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APPLICANT: Wyeth
APPLICANT: Hower
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Lowes, Steve
TITLE OF INTENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REFERENCE: 031896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
CURRENT APPLICATION NUMBER: US 60/471,729
PRIOR PILING DATE: 2004-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5571
LENGTH: 21
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CURRENT PILING DATE: 20004-05-19
CURRENT FILING DATE: 20004-05-19
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 6071
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Score 16.4; DB 1; Length 21;
Pred. No. 26;
0; Mismatches 1; Indels
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APPLICANT: Martinez, Robert
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REPERRNCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT APPLICATION NUMBER: US/10/751,736
FRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
PRIOR APPLICATION NUMBER: US
PRIOR PAPLICATION NUMBER: 303-01-06
NUMBER OF SEQ ID NOS: 54873
SOFTWARE: Patentin version 3.2
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APPLICANT: Wheth
APPLICANT: Bartinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
FITLE OF INVENTION: CANCERS
FILE OF INVENTION: CANCERS
FILE OF INVENTION: CANCERS: 203000)
CURRENT PAPLICATION NUMBER: US/10/751,736
CURRENT PILING DATE: 2003-01-06
PRIOR PILING DATE: 2003-01-06
PRIOR FILING DATE: 2003-01-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 15.2; DB
; Pred. No. 35;
0; Mismatches
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Publication No. US20040265230A1
GENERAL INFORMATION:
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US-10-731-736-17280/c
Sequence 17280, Application US/10751736
; Publication No. US20040265230A1
                                                                           sequence 9539, Application US/10751736 Publication No. US20040265230A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AACTCTGGAGTCCTCTGAGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 AACTCAGGAGTCCTGAGAGA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.7%;
Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 54873
SOFTWARE: Patentin version 3.2
SEQ ID NO 16743
LENGTH: 21
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Best Local Similarity
Matches 16; Conserva
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                                           RESULT 41
US-10-751-736-9539/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-9539
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                                                                                            ; Sequence 9539
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Publication No. US20050202431A1

GENERAL INFORMATION:

APPLICANT: Director-General of National Institute of Advanced Industrial Scie

APPLICANT: nce and Technology; Info Genes Co., Ltd.; Kazusa DNA Research Institute

TITLE OF INVENTION: Application of KIAA0172 gene functions for therapeutics, diagnosi;

TITLE OF INVENTION: and pharmaceuticals

TITLE OF INVENTION: and pharmaceuticals

FILE REPRENCE: PH-1610-PCT

CURRENT APPLICATION NUMBER: US/10/509,738

CURRENT FILING DATE: 2004-09-30

FRIOR FILING DATE: 2002-04-01

NUMBER OF SEQ ID NOS: 49

SEQ ID NOS: 49

SEQ ID NO 15

LENGTH: 22
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bo, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Slonim, Donna
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
FILE REPERENCE: 031896-026000 (AMI01264)
CURRENT APPLICATION NUMBER: US/10/847,918
PRIOR PILIAGATION NUMBER: US/10/847,918
PRIOR PILIAGATION NUMBER: US 60/471,729
PRIOR PILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 5570
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 22;
  DB 1; Length 21;
                                                1; Indels
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; Score 16.4; DB
; Pred. No. 26;
3; Mismatches
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                                                                                                                                                                                                                                                       Sequence 5570, Application US/10847918 Publication No. US20050119210A1 GENERAL INFORMATION: APPLICANT: Wyeth
                                                                                                                         2 AGCCAGCGACGCUGAUGU 19
                                                                                              51 AGCCAGCGAAGCTGATGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 GCCAGCGAAGCTGATGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
ch 21.3%;
il Similarity 77.8%;
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: RNAi-sense strand US-10-847-918-5570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.5'
Matches 13; Conservative
  Query Match
Best Local Similarity
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US-10-847-918-5570
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US-10-509-738-15
                                                  Matches
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
PILE REPERENCE: AEOMICA-7.
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT PILING DATE: 2001-05-25
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Best Local Similarity 77.8%; Pred. No. 39;
Matches 14; Conservative 2; Mismatches
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PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: PCT/USO1/00666
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00669
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: US 60/24,687
PRIOR PELICATION NUMBER: US 60/266,860
PRIOR PELIC
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Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                49 AGAGCCAGCGAAGCTGAT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AAAGCCAGCGACGCUGAU 20
PRIOR FILING DATE: 2003-05-20
NUMBER OF SEQ ID NOS: 14937
SOFTWARE: Patentin version 3.2
SEQ ID NO 2564
LENGTH: 21
                                                                                                                                                                  TYPE: RNA
CRGANISM: RNA1-sense strand
US-10-847-918-5564
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; ORGANISM: Homo sapiens
US-09-866-108-10026
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US-10-679-366-14/c
US-10-679-366-14/c
US-10-679-366-14/c
Sequence 14, Application US/10679366
Publication No. US20050059025A1
GENERAL INFORMATION:
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
TITLE OF INVENTION: KINASE
TITLE OF INVENTION: MINASE
FILE REFERENCE: MINIOTOTO
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APPLICANT: Wyeth
APPLICANT: Be, Xiaobing
APPLICANT: Liu, Wei
APPLICANT: Liu, Wei
APPLICANT: Howes, Steve
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
TILE REFERENCE: 201896-026000 (AM101264)
CURRENT APPLICATION NUMBER: US/10/847,918
PRIOR APPLICATION NUMBER: US 60/471,729
                                                                  APPLICANT: Martinez, Robert
APPLICANT: Martinez, Robert
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND WETHODS FOR DIAGNOSING AND TREATING COLON
TITLE OF INVENTION: CANCERS
FILE REPERENCE: AM100927 (031896-002000)
CURRENT APPLICATION NUMBER: US/10/751,736
CURRENT FILING DATE: 2003-01-06
FRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
FRIOR PILING DATE: 2003-01-06
NUMBER OF SEQ ID NOS: 54873
SSG ID NO 17280
LENGTH: 21
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CURRENT FILING DATE: 2003-10-07
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
LENGTH: 21
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Publication No. US20050119210A1
GENERAL INFORMATION:
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Homo sapiens
US-10-679-366-14
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Best Local Similarity
Matches 16; Conserv
             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-17280
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Sequence 10027, Application US/09866108

Fatent No. US20020048800A1

GREREAL HYCKARATION

APPLICANT: 01, Yizhong

APPLICANT: 01, Yizhong

APPLICANT: 01, Yizhong

APPLICANT: HANK, David K.

APPLICANT: CHRN WASH-11KE GRNE EXPRESSED IN HUMAN HEART AND MUSCLE FILE OF INTERFACE AND K.

FILE OF INVENTION WASH. US 00/05-25

FRIOR PLING DATE: 2001-00-4

FRIOR PLING DATE: 2001-01-30

FRIOR PLING DATE: 200
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                                    1; Indels
                                 0; Mismatches
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SOFTWARE: Acomica Sequence Listing Engine
   Pred. No.
                                                                                                27 TCTGGAGTCCTCTGAG 42
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93.8%;
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Best Local Similarity 93.8 Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-866-108-10027
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RESULT 48 US-10-723-361-10026

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GREARAL INCOMMATION:

APPLICANT: GU, Yizhong

APPLICANT: BIAN Sharron G.

APPLICANT: RANK David K.

APPLICANT: HANZEL, David K.

APPLICANT: HANZEL, David K.

APPLICANT: GREW Wensheng

APPLICANT: GREWNOWN MARK

ITILE OF INVERTION: HUMAN WOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI

FILE REFERENCE: PB0105

CURRENT PLILNG DATE: 2001-05-25

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-06-26

PRIOR PLILNG DATE: 2000-06-40

PRIOR PLILNG DATE: 2000-06-40

PRIOR PLILNG DATE: 2000-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR PLILNG DATE:
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APPLICANT: J', Yonggang
APPLICANT: J', Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
PILE REFERENCE: PB0105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
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Publication No. US20040137589A1
GENERAL INFORMATION:
Sequence 10026, Application US/10723361 Publication No. US20040137589A1
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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US-10-723-361-10027
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GENERAL INFORMATION:

APPLICANT: GU, Yalahong
APPLICANT: GU, Yalahong
APPLICANT: GU, Yalahong
APPLICANT: GU, Yalahong
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: RANK, David R.
APPLICANT: GHEN, Wencheng
APPLICANT: GHEN, Wencheng
APPLICANT: GHEN, Wencheng
APPLICANT: GHEN, WENCHOLA-1
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ADOULCA-7
CURRENT PILING DATE: 2001-05-26
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/206
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-00-30
PRIOR PILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 10024
LENGTH: 17
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PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-09-21
PRIOR PLING DATE: 2001-09-21
PRIOR PLING DATE: 2001-09-21
PRIOR PLING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SSOT DATE: 10025
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Patent No. US20020048800Al
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-866-108-10024
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APPLICANT: GI, Yizhong
APPLICANT: PENW. Sharron G.
APPLICANT: PENW. Sharron G.
APPLICANT: PENW. Sharron G.
APPLICANT: PENW. Sharron G.
APPLICANT: ANYEL, David R.
APPLICANT: RANKEL, David R.
APPLICANT: RANKEL, David R.
APPLICANT: RANKEL, David R.
APPLICANT: STANNON, Mark
ITLER OF INVERTION: MYOBEN: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
PRIOR PILING DATE: 2000-10-46
PRIOR PLING DATE: 2000-10-49
PRIOR PLING DATE: 2010-01-30
PRIOR PLING DATE: 2010-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00669
PRIOR PPLICATION NUMBER: PCT/US01/00669
PRIOR PLING DATE: 2010-01-30
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                  PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-09-27

PRIOR PLIING DATE: 2000-09-27

PRIOR PLIING DATE: 2000-09-27

PRIOR PLIING DATE: 2000-01-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLIING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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Best Local Similarity 93.8%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches
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; Patent No. US20020048800A1
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US-09-866-108-10024
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APPLICANT: PENN, Shārron G.
APPLICANT: HANZEL, David K.
APPLICANT: HANXEL, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: STANNON, Mark
TITLE OP INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
FILE REFERENCE: P80105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Sequence 930, Application US/10060998

Publication No. US20030104530A1

SEQUENCE INFORMATION:

APPLICANT:

APPLICANT:

STILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/060, 998

CURRENT FILING DATE: 2002-01-30

FRIOR PAPLICATION NUMBER: PCT/US01/00666

PRIOR PILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-05-23

FRIOR FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 3056

SEQ ID NO 930

LENGTH: 17
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SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 10025
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                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR PLILING DATE: 2001-05-26
PRIOR PELING DATE: 2001-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-10-30
PRIOR PLLING DATE: 2000-10-30
PRIOR PLLING DATE: 2000-10-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
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US-10-060-998-930
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Best Local Similarity
Matches 14; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10024, Application US/10723361
Publication No. US20040137589A1
GENERAL INFORMATION:
APPLICANT: GU, YIZADOG
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANKON, Mark
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
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CURRENT APPLICATION NUMBER: US/10/723,361

CURRENT FILING DATE: 2003-11-26

FRIOR PEDICATION NUMBER: US 09/866,108

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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                                                                                                                       Query Match 18.2%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 34; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                  27 TCTGGAGTCCTCTG 40
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                             ; ORGANISM: Homo sapiens
US-09-866-108-10025
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Best Local Similarity
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US-10-723-361-10025
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LENGTH: 17
TYPE: DNA
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-10-060-998-931
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                      Gaps
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Pred. No. 40;
0; Mismatches 1; Indels
                                      2; Indels
Best Local Similarity 88.2%; Pred. No. 36; Matches 15; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT PILING DATE: 2001-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-07

PRIOR PILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR PILING DATE: 2001-01-30

PRIOR P
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Patent No. US20020048800A1
                                                                                             47 AAAGAGCCAGCGAAGCT 63
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                                                                                                                                                      17 AATGAGCCAGCGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-10028
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Best Local Similarity
Matches 14; Conserva
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US-10-060-998-931/c
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Publication No. US20030104530A1

SEGREAL INFORMATION:

APPLICANT: Gu, YiZhong

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPERBNCE: PB01108

CURRENT PELLING DATE: 2002-01-30

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: US 09/864,761

FRIOR APPLICATION NUMBER: US 09/864,761

FRIOR APPLICATION NUMBER: US 09/864,761

FRIOR PILING DATE: 2001-05-23

FRIOR PILING DATE: 2001-10-52

NUMBER OF SEQ ID NOS: 3056

SEQ ID NO 932

LENGTH: 17
; Sequence 931, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; CURRENT APPLICATION NUMBER: US/10/066, 998
; CURRENT FILING DATE: 2002-01-30
; PRIOR PPLICATION NUMBER: PCT/US01/00666
; PRIOR PLILING DATE: 2001-05-23
; PRIOR PLILING DATE: 2001-05-23
; PRIOR PLILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Asomica Sequence Listing Engine
; SEQ ID NO 931
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Pred. No. 40;
0; Mismatches
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US-10-723-361-10028

Sequence 10028, Application US/10723361

Publication No. US20040137589A1

GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: HANZEL, David K.
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JARDICANT: Corvas International, Inc.
APPLICANT: Madison, Edwin L.
APPLICANT: Semple, Joseph Bdward
APPLICANT: Semple, Joseph Bdward
APPLICANT: Semple, Joseph Bdward
APPLICANT: Coombs, Gary Samuel
APPLICANT: Coombs, Gary Samuel
APPLICANT: Araldi, Gian Luca
APPLICANT: Araldi, Gian Luca
TITLE OF INVENTION: Inhibitors of Serine Protease Activity of Matriptase or MTSP1
TILE REFERENCE: 018813/0282105
CURRENT APPLICATION NUMBER: US/10/092,004A
CURRENT FILING DATE: 2001-09-07
FRIOR APPLICATION NUMBER: PCT/US01/28137
FRIOR FLING DATE: 2001-09-07
FRIOR APPLICATION NUMBER: 09/657,986
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANKEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: GHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
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                                                                                                                                                                                                                                                                                             Query Match
17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                         ; OTHER INFORMATION: Oligonucleoide Primer US-09-776-191-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/207,456
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LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-10-092-004A-6/C
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                               APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
FILE REFERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT PILING DATE: 2003-11-26
PRIOR PILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-27
PRIOR PLING DATE: 2000-05-27
PRIOR PLING DATE: 2001-01-30

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Sequence 56, Application No. US20030119168A1

GENERAL INFORMATION:
APPLICANT: Edwin L.
APPLICANT: Edwin L.
APPLICANT: Edwin L.
APPLICANT: Alumn-Chern Yeh
APPLICANT: Graves International, Inc.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: TRANSMEMBRANE SERINB PROTEASES, THE ENCODED PROTEINS AND
TITLE OF INVENTION: METHODS BASED THEREON
CURRENT APPLICATION NUMBER: 60/213,124
PRIOR PELING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/134,840
PRIOR PILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/179,982
PRIOR PILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 60/183,542
PRIOR APPLICATION NUMBER: 60/183,542
PRIOR APPLICATION NUMBER: 09/657,968
PRIOR PILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/657,968
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NUMBER OF SEQ ID NOS: 72
SEQTYARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
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ORGANISM: Homo sapiens
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US-09-776-191-56/c
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| Sequence 11, Application US203028592A1
| Fublication No. US20030228592A1
| GENERAL INFORMATION:
| APPLICANT: St Vincent's Institute of Medical Research
| APPLICANT: Rogers, Susanne D
| APPLICANT: Rogers, James D
| TITLE OF INVENTION: Human Pacilitative Glucose Transport Protein GLUT8
| TITLE OF INVENTION: Human Pacilitative Glucose Transport Protein GLUT8
| TILE OF INVENTION: Human Pacilitative Glucose Transport Protein GLUT8
| TILE REFERENCE: VS.A.H.:PP1728
| CURRENT PILING DATE: 2003-02-19
| PRIOR FILING DATE: 2003-02-19
| NUMBER OF SEQ ID NOS: 42
| SEQ ID NO 11
| LENGTH: 18
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                                                                      PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-0
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Publication No. US20030104530A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GU, YIZHONG
TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
FILE REFERENCE: P801108
CURRENT PELLING DATE: 2002-01-30
CURRENT FILING DATE: 2002-01-30
PRIOR PILING DATE: 2001-01-30
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                 LING DATE: 2001-01-30
PLICATION NUMBER: PCT/US01/00664
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; OTHER INFORMATION: PCR primer (reverse)
US-10-367-980A-11
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-10-723-361-10023
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APPLICANT: PRNN, Sharron G.
APPLICANT: HANGEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wencheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR PELING DATE: 2003-11-26
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-10-04
PRIOR PLLING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PRIOR DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 TCTGGAGTCCTCT 39
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Best Local Similarity 100.
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-10023
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APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Rarpeisky, Alex
APPLICANT: Karpeisky, Alex
APPLICANT: Shadmic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot:
FILE REPERENCE: MEHBOO-831-F (400/009)
CURRENT APPLICATION NUMBER: US/09/825,805
CURRENT FILING DATE: 2001-09-27
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                     PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: PCT/USO1/0066
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PERIOR DATE: 2001-01-30
PRIOR PELING DATE: 20
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Publication No. US20030004122A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 09/476, 387
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
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PRIOR APPLICATION NUMBER: 09/186,675
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-825-805-816
    CURRENT
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Sequence 7, Application US/10469277

Publication No. US20040170996A1

GENERAL INFORMATION:
APPLICANT: Yee, Leland
APPLICANT: Raslow, Bichard A.
APPLICANT: Raslow, Bichard A.
APPLICANT: Was Leewen, Dirk J.
ITILE OF INVENTION: AS PREDICTORS OF RESPONSE TO THERABEUTIC INTERVENTION
FILE OF INVENTION: AS PREDICTORS OF RESPONSE TO THERAPEUTIC INTERVENTION
CURRENT APPLICATION NUMBER: US/10/469,277

CURRENT PILING DATE: 2003-08-27

PRIOR PLLING DATE: 2002-02-27

PRIOR PLLING DATE: 2001-02-27

SPRIOR PLLING DATE: 2001-02-27

NUMBER OF SEQ ID NOS: 10

SOUTHARE: PatentIn version 3.2

SEQ ID NO 7

LENTHER PATENTER PATENT
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APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
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Best Local Similarity 87.5%; Pred. No. 52;
Matches 14; Conservative 0; Mismatches
                                                                                                                                                             NUMBER OF SEQ ID NOS: 3056
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 929
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Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GI, Yiahong
APPLICANT: JI, Yonggang
APPLICANT: FENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: GHRW, Wensheng
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/343,331
PRIOR PILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Reverse primer US-10-469-277-7
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US-10-060-998-929
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ORGANISM: Artificial
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US-09-866-108-10029
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50 GAGCCAGCGAAGCT 63
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                                             TYPE: DNA
CRGANISM: Homo sapiens
US-10-060-998-928
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; ORGANISM: Homo sapiens
US-10-060-998-933
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US-10-163-552-786
                                                                                                                                                                                                                                                                                                                                                                            US-10-060-998-933/c
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       SEQ ID NO 928
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| Publication No. US20030104530A1
| GENERAL INPORMATION:
| APPLICANT: GU, YIZhong
| TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
| FILE REPRENCES: PB01108
| CURRENT APPLICATION NUMBER: US/10/060,998
| CURRENT PILING DATE: 2002-01-30
| PRIOR PEPLICATION NUMBER: PCT/US01/00666
| PRIOR PAPPLICATION NUMBER: US/0804,761
| PRIOR APPLICATION NUMBER: US 60/343,331
| PRIOR APPLICATION NUMBER: US 60/343,331
| PRIOR PILING DATE: 2001-05-23
| PRIOR PILING DATE: 2001-05-23
| PRIOR PILING DATE: 2001-15-13
| NUMBER OF SEQ ID NOS: 3056
| SOFTWARE: Aeomica Sequence Listing Engine |
| LENGTH: 17
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Publication No. US20030104530A1
GENERAL INFORMATION:
APPLICANT: GL, YIZADOG
TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
FILE REFERENCE: PB01108
CURRENT PLING DATE: 2002-01-30
FRIOR APPLICATION NUMBER: US/10/0666
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR APPLICATION NUMBER: US 09/864,761
FRIOR APPLICATION NUMBER: US 09/864,761
FRIOR PILING DATE: 2001-02-23
FRIOR FILING DATE: 2001-01-20
FRIOR FILING DATE: 2001-12-21
MUMBER OF SEQ ID NOS: 3056
SOFTWARE: Acomica Sequence Listing Engine
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Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches
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Pred. No. 52;
3; Mismatches
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR PILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1558
SOFTWARE PATENTIN VETSION 3.0
SEQ ID NO 816
LENGTH: 17
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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US-09-825-805-816
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US-10-060-998-927
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US-10-060-998-927/c
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Sequence 786, Application US/10163552

Publication No. US20030105051A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Here2

TITLE OF INVENTION: Here2

TITLE OF INVENTION: Here2

CURRENT APPLICATION NUMBER: US/10/163,552

CURRENT FILING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 1997

SOFTWARE: Patentin version 3.0

SEQ ID NO 786

LENGTH: 17
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                                                                                                                                                                                                                                                               Publication No. US20030104530A1
| Publication No. US20030104530A1
| GRARRAL INPORMATION:
| APPLICANT:
| GUNERAL INPORMATION:
| TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
| FILE REFERENCE:
| CURRENT APPLICATION NUMBER: US/10/060,998
| CURRENT PILING DATE: 2002-01-30
| PRIOR APPLICATION NUMBER: PCT/US01/00666
| PRIOR PILING DATE: 2001-01-30
| PRIOR PILING DATE: 2001-01-30
| PRIOR PILING DATE: 2001-05-23
| PRIOR PILING DATE: 2001-12-13
| NUMBER OF SEQ ID NOS: 3056
| SEQ ID NOS: 3056
| SEQ ID NO 933
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Best Local Similarity 92.8%; Pred. No. 52,
Matches 13; Conservative 0; Mismatches 1. Tran.
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Pred. No. 52;
3; Mismatches 1; Indels
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Pred. No. 52;
0; Mismatches
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Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 71.4%;
Matches 10; Conservative
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APPLICANT: OL, ITAIDONG
APPLICANT: OL, ITAIDONG
APPLICANT: OL, YONGGANG
APPLICANT: PENN, Sharron G.
APPLICANT: PRNK, Sharron G.
APPLICANT: PRNK, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANKON, MARK
TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
TITLE OF INVENTION: HUMAN WASIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
CURRENT FILING DATE: 2003-11-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PPLICATION NUMBER: BC7/US01/0066
PRIOR PELICATION NUMBER: PC7/US01/0066
PRIOR PELICATION NUMBER: PC7/US01/0066
PRIOR PELICATION NUMBER: PC7/US01/0066
PRIOR APPLICATION NUMBER: PC7/US01/0066
PRIOR APPLICATION NUMBER: PC7/US01/0066
PRIOR PELICATION NUMBER: PC7/US01/0066
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APPLICANT: Sandberg, Jennifer
APPLICANT: Sandberg, Jennifer
APPLICANT: School, Jennifer
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTY
TITLE OF INVENTION: NUCLEIC 400, 047)
CURRENT APPLICATION NUMBER: US,10/712,633
CURRENT APPLICATION NUMBER: US,60/005,974
PRIOR FILING DATE: 1995-10-26
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SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 10029
LENGTH: 17
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; Publication No. US20040220128A1
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
PRIOR PILING DATE: 2000-11-07
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Best Local Similarity 92.9
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-10-723-361-10029
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Sequence 714, Application US/10287949A

Publication No. US20040102389A1

Sequence 714, Papication No. US20040102389A1

Sequence 714, Application No. US20040102389A1

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH800-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 20822

SOUTHARE: Patentin version 3.0

SEQ ID NO 7914

LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Recept
FILE REPERENCE: MBHB00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 2002-05-03
SOFTWARE: Patentin version 3.0
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64.3%; Pred. No. 52;
tive 4; Mismatches
                                                                                                                                                                                              Sequence 7914, Application US/10138674; Publication No. US20040077565A1; GENERAL INFORMATION; APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: Pavco, Pam APPLICANT: McSwiggen, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 74
US-10-723-361-10029
Sequence 10029, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
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cucggcAguccucu 15
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cucggaAguccucu 15
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Best Local Similarity 64.37
Best Local Similarity 64.37
Conservative
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Matches 9, Conservative
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US-10-138-674-7914
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Stinchcomb, Dan
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Expansion of NF-Kappa B
TITLE OF INVENTION: Levels of NF-Kappa B
TITLE REFERENCE: 400/022 (MBHB00-812-D)
CURRENT APPLICATION NUBBRS: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
SOFTWARET PatentIn version 3.0
SEQ ID NO 2825
LENGTH: 17
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Publication No. US20030092003A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease FILE REFERENCE: MSWIGGEN, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease CURRENT APPLICATION NUMBER: US/09/930, 423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: Patentin version 3.0
SEQ ID NO 1056
LENGTH: 17
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Sequence 1056, Application US/09745237A
Publication No. US20030143708A1
GENERAL INPORMATION:
APPLICANT: Blatt, Larry
APPLICANT: MCSWAGGGH, Jim
APPLICANT: MCSWAGGH, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease;
FILE REFERENCE: 400/007 (MBHB00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Best Local Similarity 58.8%; Pred. No. 55;
Matches 10; Conservative 4; Mismatches
                                                                             Sequence 2825, Application US/09864785
Patent No. US20020177568A1
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ORGANISM: Artificial Sequence
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CRGANISM: Homo Sapiene
US-09-930-423-1056
                                             IS-09-864-785-2825/C
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Sequence 5441, Application US/10724270

Fublication No. U52050000031A1

Publication No. U52050000031A1

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: No. U5205-11-26

FILE REFERENCE: 400/404-218 (MEMBRO 2-326-A)

CURRENT APPLICATION NUMBER: US/10/724, 270

CURRENT APPLICATION NUMBER: US/10/21/6840

PRIOR FILING DATE: 2001-05-10

PRIOR PILING DATE: 2001-05-20

PRIOR PILING DATE: 2001-05-20

PRIOR PILING DATE: 2001-05-30

PRIOR PRIOR PILING DATE: 2001-05-30

PRIOR PRIOR PRILING DATE: 2001-05-30

PRIOR PRIOR PRILING DATE: 2001-05-30

PRIOR PRINCE DATE: 2001-05-30

PRIOR PRINCE DATE: 2001-05-30

PRIOR PRINCE DATE: 2
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Pred. No. 52;
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PRIOR APPLICATION NUMBER: US US/O///LLP PRIOR FILING DATB: 2001-05-29
PRIOR APPLICATION NUMBER: US 60/334,461
PRIOR PILING DATB: 2001-11-30
PRIOR PILING DATB: 2001-11-30
PRIOR PILING DATB: 2002-05-03
NUMBER OF SEQ ID NOS: 5989
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA; ORGANISM: Homo Sapiens
US-10-712-633-1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-724-270-5441
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APPLICANT: Ravoco, Pamela
APPLICANT: Ravoco, Pamela
APPLICANT: Sandberg, Jennifer
APPLICANT: Gardon, Glad
APPLICANT: Grandb, Dan
TITLE OF INVENTION: UNCLERC ALGID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND CURRENT FILING DATE: 1995-10-13
FILE REFERENCE: MBHB02-325PCT (400/047)
CURRENT FILING DATE: 1995-10-26
FRIOR APPLICATION NUMBER: US 06/005,974
FRIOR PILING DATE: 1996-01-08
FRIOR APPLICATION NUMBER: US 09/371,772
FRIOR APPLICATION NUMBER: US 09/371,772
FRIOR APPLICATION NUMBER: US 09/371,772
FRIOR APPLICATION NUMBER: US 09/371,61
FRIOR PILING DATE: 2000-11-07
FRIOR PILING DATE: 2001-05-29
FRIOR PILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
FRIOR FILING DATE: 2002-05-30
FRIOR FILING DATE: 2002-05-03
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15.8%; Score 12.2; DB 1; Length 17; 82.4%; Pred. No. 55;
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; Sequence 108, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
; APPLICANT: Galdzicka, Marzena
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
; TITLE OF INVENTION: SYSTEMS AND WETHODS FOR ANALYZING
; TITLE OF INVENTION: SYSTEMS AND WETHODS FOR ANALYZING
; TITLE OF INVENTION: SYSTEMS AND WETHOR SEQUENCES
; FILE REPERENCE: 07917-238001
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/493,238
; PRIOR APPLICATION NUMBER: US 60/568,958
; PRIOR PILING DATE: 2003-08-06
; PRIOR PILING DATE: 2003-08-06
; PRIOR PILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 920
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Pred. No. 55;
0; Mismatches
                                                          0; Mismatches
                                                                                                                                                                                                                                                          RESULT 82
US-10-712-633-4058/c
i Sequence 4058, Application US/10712633
i Publication No. US20040220128A1
i GENERAL INFORMATION:
i APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                  60 AGCTGATGTCCTGTCAA 76
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                          14; Conservative
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US-10-712-633-4058
                          Best Local Similarity
Matches 14; Conserve
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     Query Match
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publication No. US20040102389A1

GENERAL INFORMATION:
APPLICANT: Pavco, Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MEMBRO-976-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A

CURRENT FILING DATE: 2003-04-11

SOFTHARE: Patentin version 3.0

SSO ID NO 8872

LENGTH: 17
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; Sequence 8872, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Bavco, Pam

; APPLICANT: Bavco, Pam

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditi;
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/49)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NOWBER OF SEQ ID NOS: 20822
; SOFTMARE: Patentin version 3.0
; SEQ ID NO 8872
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Best Local Similarity 82.4%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                             Query Match 15.8%; Score 12.2; I
Best Local Similarity 58.8%; Pred. No. 55;
Matches 10; Conservative 4; Mismatches
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: Patentin version 3.0
SEQ ID NO 1056
LENGTH: 17
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CORGANISM: Homo sapiens
US-10-138-674-8872
                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-745-237A-1056
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; ORGANISM: Homo sapiens
US-10-287-949A-8872
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Squence 593, Application US/10776934

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Squence 593, Application US/10776934

Squence 593, Application US/20050014712A1

GENERAL INPORMATION:

APPLICANT: HANSEN, BO

APPLICANT: WESTERGARD, MAJKEN

APPLICANT: WISSENBACH, MARKEN

APPLICANT: WISSENBACH, MARKEN

TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: 58610/71432)

CURRENT APPLICATION NUMBER: 00/446,372

PRIOR APPLICATION NUMBER: 60/446,372

PRIOR APPLICATION NUMBER: 60/523,591

PRIOR PILING DATE: 2003-11-19

NUMBER OF SEC ID NOS: 741

SQCIWARR: PatentIn version 3.2

SEC ID NO 593

LENGTH. 16
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                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(4) OTHER INFORMATION: beta-D-oxy-LNA modified base FEATURE:
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LOCATION: (1)..(4)
OTHER INFORMATION: beta-D-oxy-LNA modified base
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LOCATION: (13)..(15)
OTHER INFORMATION: beta-D-oxy-LNA modified base
                                                                                                                                           FRATURE: OTHER INFORMATION: Synthetic oligonucleotide
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    i LOCATION: (1)..(16)
    i OTHER INFORMATION: phosphorthioate linkage
    i 10-776-934-593

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100.0%; Pred. No.
NUMBER OF SEQ ID NOS: 741
SOFTWARE: Patentin version 3.2
SEQ ID NO 522
LENGTH: 16
                                                                                            TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial sequence
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                                                                                                                                                                                         FEATURE:
NAME/KEY: modified_base
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Best Local Similarity
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US-10-776-934-593
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APPLICANT: TERUS, CHARLOTTE ALBABEK
APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: WESTERGAARD, MAJKEN
APPLICANT: WISSENBACH, WARGIT
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENT APPLICATION NUMBER: US/10/776,934
CURRENT PILLING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/446,372
PRIOR FILING DATE: 2003-02-10
PRIOR PILING DATE: 2003-01-19
NUMBER OF SEQ ID NOS: 741
SOFTWARE: Patentin version 3.2
SEQ ID NO 113
LENGTH: 16
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APPLICANT: THRUE, CHARLOTTE ALBAEK
APPLICANT: PETERGARD, MAJKEN
APPLICANT: PETERGARD, MAJKEN
APPLICANT: WISSENBACH, KAMILLE DUNONG
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: 58610(71432)
CURRENT APPLICATION NUMBER: 60/10/776,934
CURRENT FILING DATE: 2004-02-10
PRIOR PLILING DATE: 2003-02-10
PRIOR PLILING DATE: 2003-01-10
PRIOR PLILING DATE: 2003-11-19
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15.8%; Score 12.2; D.
Best Local Similarity 82.4%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic oligonucleotide US-10-776-934-113
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // Bequence 113, Application US/10776934
// Publication No. US20050014712A1
// GENERAL INFORMATION:
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Publication No. US20050014712A1
GENERAL INFORMATION:
APPLICANT: HANSEN, BO
APPLICANT: THRUE, CHARLOTTE ALBAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HANSEN, BO
APPLICANT: THRUE, CHARLOTTE ALBAEK
                                                                                                                                                                                                                                                                                                                                  1 ACACAGGCGTCCTCTGA 17
                                                                                                                                                                                                                                                                                                          25 ACTCTGGAGTCCTCTGA 41
                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                        OTHER INFORMATION: Primer US-10-913-280-108
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                                                                                                                       FEATURE:
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GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: FINN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: GHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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53;
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OTHER INFORMATION: Synthetic oligonucleotide
FEATURE:
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PRIOR PLICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/205,266
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-07
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
; LOCATION: (1)...(16)
... OTHER INFORMATION: phosphorthioate linkage
US-10-776-934-595
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CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 12; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10022, Application US/09866108 Patent No. US20020048800A1
                        NUMBER OF SEQ ID NOS: 741
SOFTWARE: Patentin version 3.2
SEQ ID NO 595
LENGTH: 16
                                                                                                                                            TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 CCAGCGAAGCTG 64
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US-09-866-108-10022
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                                                                                                                                                                                                                                          Sequence 594, Application US/10776934

| Bedication No. US20050014712A1
| GENERAL INCOMMATION:
| APPLICANT: HANSEN BO
| APPLICANT: THRUE, CHARLOTTE ALBAEK
| APPLICANT: THRUE, CHARLOTTE ALBAEK
| APPLICANT: WISSENBACH, MARGIT
| TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
| TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
| FILE REFERENCE: 58610(71432)
| CURRENT APPLICATION NUMBER: 05/10/76,934
| CURRENT APPLICATION NUMBER: 60/446,372
| PRIOR PILING DATE: 2003-02-10
| PRIOR FILING DATE: 2003-01-19
| PRIOR FILING DATE: 2003-11-19
| NUMBER OF SEQ ID NOS: 741
| SOFTWARE: Patentin version 3.2
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| Publication No. US20050014712A1 |
| GENERAL INFORMATION |
| APPLICANT: HANSEN, BO |
| APPLICANT: HANSEN, BO |
| APPLICANT: HESTERGARD, MAJKEN |
| APPLICANT: PETERSEN, KAMILLE DUWONG |
| APPLICANT: PETERSEN, KAMILLE OF 1000MERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION |
| TITLE OF INVENTION OF 1004-02-10 |
| CURRENT PILING DATE: 2004-02-10 |
| PRIOR APPLICATION NUMBER: 60/446,372 |
| PRIOR APPLICATION NUMBER: 60/523,591 |
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   Gaps
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Indels
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LOCATION: (13)..(15)
OTHER INFORMATION: beta-D-oxy-LNA modified base
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LOCATION: (1)..(4)
OTHER INFORMATION: beta-D-oxy-LNA modified base
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0; Mismatches
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; IOCATION: (5)..(13)

; OTHER INFORMATION: phosphorthioate linkage

US-10-776-934-594
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ORGANISM: Artificial sequence
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Best Local Similarity 100.
12; Conservative
                                                         53 CCAGCGAAGCTG 64
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US-10-776-934-594
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US-10-776-934-595
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Matches
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APPLICANT: waxed, Pam
APPLICANT: McSariggen, Jim
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Mymber: US/10/43)
CURRENT APPLICATION NUMBER: US/10/43)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT PILLING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 2002-05-03
SOFTWARE: Patentin version 3.0
END NO 6986
LEMPIT: 16
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### APPLICANT:

### APPL
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Sequence 73537, Application US/10741600

Sublication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: 030140499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT PILING DATE: 2003-12-22

NUMBER OP SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 73537
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Pred. No. 55;
0; Mismatches
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Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.3%;
Best Local Similarity 86.7%;
Matches 13; Conservative (
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Best Local Similarity 86.7%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-287-949A-6986
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                                                                                                                                                                                                                                                          15.6%; Score 12; DB 1; Length 17; 100.0%; Pred. No. 58; cive 0; Mismatches 0; Indels
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; Publication No. US20040137589A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
                                                                                                                                                                                                                                                          Query Match 15.6
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                  27 TCTGGAGTCCTC 38
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                                                                                                                                                 TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10022
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US-10-138-674-6986/c
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                                                                                                                              LENGTH: 17
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Sequence 184441, Application US/10257017B
Publication No. US20040241651A1
Publication No. US20040241651A1
Publication No. US20040241651A1
Sequence 184441, Application No. US20040241651A1
APPLICANT: Alexander Olek
APPLICANT: Christlan Piepenbrock
APPLICANT: Christlan Piepenbrock
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
APPLICANT: Murt Berlin
APPLICANT: WINGHER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICANTON NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICANTON NUMBER: DE 10019173.8
PRIOR APPLICANTON NUMBER: DE 10019173.8
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i Sequence 184442, Application US/10257017B

i Publication No. US20040241651A1

i CBNERAL INFORMATION:

APPLICANT: Alexander Olek

i APPLICANT: Christian Piepenbrock

APPLICANT: Christian Piepenbrock

TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine

TITLE OF INVENTION: methylations

FILE REFERENCE: E01/1193/WO

CURRENT APPLICATION WUMBER: US/10/257,017B

CURRENT APPLICATION WUMBER: DE 10019173.8

PRIOR PILING DATE: 2002-10-07

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 382046

SEQ ID NO 184442
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045516
US-10-257-017B-184441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045516
US-10-257-017B-184442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Length 13
   Indels
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No. 43;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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SEQ ID NO 184441
LENGTH: 13
                                                                39 TGAGAGGTAAAGA 51
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Best Local Similarity 92.3
Matches 12; Conservative
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   12; Conservative
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13 TGAGATGTAAAGA 1
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US-10-257-017B-18441
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Matches
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Sequence 41877, Application US/10257017B

Publication No. US20040241651A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Poetection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
TITLE OF INVENTIONS
TITLE O
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION WUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 41788
LENGTH: 13
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US-10-257-017B-41787
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US-10-257-0178-41788
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                                                                                                                                                       Score 11.8; DB 1; Length 16;
Pred. No. 55;
0; Mismatches 2; Indels
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Pred. No. 43;
0; Mismatches
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                                                                                                                                                       15.3%;
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                                                                                                                                                                                                                                                                                     31 GAGTCCTCTGAGAGG 45
                                                                                                                                                                                                                                                                                                                                            GAGTCCTCCGGGAGG 2
                                                                                                                             Query Match
Best Local Similarity 86.77
Best Local 31 Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-73537
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 94
US-10-257-017B-41787
   LENGTH: 16
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Query Match
Best Local Similarity 80.0°
Matches 12; Conservative
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Best Local Similarity 80.0
Matches 12; Conservative
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                        Sequence 26, Application US/10142729

; Sequence 26, Application US/2030165888A1
; Sequence 26, Application Worlow US20030165888A1
; GENERAL INPORMATION:
; APPLICANT: BIOWN, BOD D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; FILE REFERENCE: OASBIO.005A
; CURRENT APPLICATION NUMBER: US/10/142,729
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR PILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR PLILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NOS: 94
; SEQ ID NO 25
; SEQ ID NO 25
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Sequence 39, Application US/10142729

PUBLIcation No. US20000165888A1

GENERAL INFORMATION:

APPLICANT: Brown, Bob D.

APPLICANT: Riley, Timothy A.

TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES

TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES

TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES

CURRENT PILING DATE: 2002-08-29

PRIOR PILING DATE: 2001-07-18

PRIOR PILING DATE: 1998-08-18

PRIOR PILING DATE: 1998-08-18

PRIOR PILING DATE: 1997-10-02

NUMBER OF SEQ ID NOS: 94

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 39

LENGUTH: 16
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Pred. No. 61;
0; Mismatches 3; Indels
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i_LOCATION: 4, 10
control inFormation: n = modified base
US-10-142-729-26
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// LOCATION: 4, 10
// OTHER INFORMATION: n = modified base
US-10-142-729-39
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.0%;
Matches 12; Conservative
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Gaps
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ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. US20030181660Alth Glebe Road, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/331,907
FILING DATE: 31-Dec-2002
PRIOR APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Reb-2001
APPLICATION NUMBER: PC/76998/01102
FILING DATE: 15-APR-1998
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
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                                                                                                                                                                            DB 1; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAWAGUCHI, Yoshihiko
Merriman, Tony R
Merzker, Michael L
TITLE OF INVENTION: No. US20030181660Alel LDL-Receptor
NUMBER OF SEQUENCES: 455
                                                                                                                                                                                                                       Indels
                                                                                                                                                                          Query Match 14.5%; Score 11.2; I
Best Local Similarity 81.2%; Pred. No. 65;
Matches 13; Conservative 0; Mismatches
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APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 450: US-10-331-907-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
NUMBER OF SEQ ID NOS: 78
SOFTWARER: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 450, Application US/10331907
Publication No. US20030181660A1
GENERAL INFORMATION:
APPLICANT: Todd, John W
Gaskey, Charles T
Cox, Roger D
Gerhold, David
Hey, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 450: SEQUENCE CHARACTERISTICS: LENGTH: 16 base pairs
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NAME: B.J.Sadoff
                                                                                                                                                                                                                                                                  38 CTGAGAGGTAAAGAGC 53
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                                                                                      TYPE: DNA
CRGANISM: Homo sapiens
US-09-875-453-65
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| Publication No. US20040265849A1
| GENERAL INPORMATION:
| APPLICAMT: CARGILL, Michele et al.
| TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/10/719,993
| CURRENT APPLICATION NUMBER: US/10/719,993
| CURRENT PILING DATE: 2003-11-24
| NUMBER OF SEQ ID NOS: 55342
| SEQ ID NO 55182
| LENGTH: 16
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TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
FILE REFERENCE: 4600-0135.30
CURRENT APPLICATION NUMBER: US/09/875,453
CURRENT FILING DATE: 2001-06-06
PRIOR PAPLICATION NUMBER: US 60/209,549
PRIOR PILING DATE: 2000-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                 FEATURE: OTHER INFORMATION: Artificial Oligonucleotide
                                                                                                                                                                                                                                                                                      ; Score 11.4; DB; Pred. No. 61; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11.4; D
Pred. No. 61;
0; Mismatches
    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 39 LENGTH: 16
                                                                                                                                                                            NAME/KEY: misc_feature; LOCATION: 4, 10; CATION: 10 TO THE INFORMATION: n = modified base US-10-375-504-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65, Application US/09875453
Publication No. US20030027320A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laurance, Megan E.
Michelotti, Emil F.
Velligan, Mark D.
Latour, Derek R.
Thomas, Rita L.
Kongpachith, Ana
Sheppard, Liana T.
Lim, Moon Young
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                                                                                                                                                                                                                                                                                           14.8%;
80.0%;
                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Starr, Douglas B.
APPLICANT: Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                        15 GATACNGCTCTNGAG 1
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo Bapiens
US-10-719-993-55182
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US-09-875-453-65/c
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APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REPERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,0178
CURRENT PILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: B 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 320928
LENGTH: 12
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Publication No. US20040241651A1
Sequence 1453), Application No. US20040241651A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms
FILE REFERENCE: 2001/1193/WO
CURRENT PILING DATE: 2002-10-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 14593
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Oligonuclectide primer for the detection of SNP TSC0029975
US-10-257-017B-320928
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                                                                                                                                                                                                                 Sequence 320928, Application US/10257017B
Publication No. US20040241651A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 11; Conservative
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20 ATACAACTCTG 30
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                                                         11 ATACAACTCTG 1
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Best Local Similarity
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US-10-257-017B-14594/c
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18-10-450-797-548/C

18 Sequence 548, Application US/10450797

28 Sequence 548, Application US/10450797

28 Publication No. US20040142335A1

38 APPLICANT: Petersohn, Dirk

3 APPLICANT: Petersohn, Marcus

3 APPLICANT: Conradt, Marcus

3 APPLICANT: Petersohn, Nameus

4 PILE REFERENCE: HENK-0041

5 CURRENT PILING DATE: 2003-12-04

5 PRIOR PILING DATE: 2001-12-20

5 PRIOR PILING DATE: 2001-12-20

5 PRIOR PILING DATE: 2001-03

6 PRIOR PILING DATE: 2001-01-03

7 NUMBER OF SEQ ID NOS: 1435

7 SEQ ID NO 548

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Sequence 67, Application No. US20040096848A1

GENERAL INFORMATION:

APPLICANT: THRUE, CHARAT

APPLICANT: HOG, ANNA MOLHART

APPLICANT: KRISTJANSEN, PAUL B.G.

TITLE OF INVENTION: OLIGGOMERIC COMPOUNDS FOR THE MODULATION HIF-IALPHA

TITLE OF INVENTION: EXPRESSION

FILE REFERENCE: 57390 (45120)

CURRENT APPLICATION NUMBER: US/10/407,807

CURRENT PILING DATE: 2003-10-25

PRIOR PILING DATE: 2003-10-25

PRIOR PILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 124

SOFTWARE: PALENTIN VET. 3.2

SEQ ID NO 67
                                                                                              Gaps
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US-10-407-807-67
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                              DB 1; Length 16;
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                                                                                              3; Indels
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14.5%; Score 11.2; DB 1;
Best Local Similarity 81.2%; Pred. No. 65;
Matches 13; Conservative 0; Mismatches 3;
                           14.5%; Score 11.2; Di
81.2%; Pred. No. 65;
tive 0; Mismatches
                                                                                                                                                               39 TGAGAGGTAAAGAGCC 54
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ORGANISM: Artificial Sequence
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16 AAACACACAGGGAAGC 1
                    Query Match
Best Local Similarity 81.2
Matches 13; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: Homo sapiens
US-10-450-797-548
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US-10-407-807-67/c
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Sequence 224917, Application US/10257017B
; Sequence 224917, Application US/10257017B
; Publication No. US20040241651A1
; Publication No. US20040241651A1
; RENEATION: APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR PILING DATE: 2000-04-07
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 224917
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Publication No. US20040241651A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: methylations
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/WO
CURRENT FILING DATE: 2002-10-07
CURRENT FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 13; 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
; TITLE OF INVENTION: methylations; FILE REFERENCE: E01/1193/WO CURRENT APPLICATION NUMBER: US/10/257,017B; CURRENT FILING DATE: 2002-10-07; PRIOR APPLICATION NUMBER: DE 10019173.8; PRIOR FILING DATE: 2000-04-07; NUMBER OF SEQ ID NOS: 382046; SEQ ID NO 181998
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                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Matches 11; Conservative
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US-10-257-017B-181998/c
; Sequence 181998, Application US/10257017B
; Sequence 181998, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
                                                                                             APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OP INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 14594
LENGTH: 13
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
TITLE OF INVENTION: methylations
FILE REFERENCE: E01/1193/W0
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 181997
LENGTH: 13
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US-10-257-017B-181997
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14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels
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; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
     Sequence 14594, Application US/10257017B Publication No. US20040241651A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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13 AGAAGTAAAGAGY 1
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                                                                                     APPLICANT: Alexander Olek
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US-10-257-017B-181997
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RESULT 116

US-09-504-231A-1178/C

1 Sequence 1178 Application US/09504231A

2 Sequence 1178 Blatt, Lawrence

3 APPLICANT: Blatt, Lawrence

3 APPLICANT: Reverse Blatt, Lawrence

3 APPLICANT: Reverse Pamela

4 APPLICANT: Reverse Pamela

4 APPLICANT: Reverse Pamela

5 APPLICANT: Reverse Pamela

5 APPLICANT: Reverse Pamela

6 APPLICANT: Reverse Pamela

7 TITLE OF INVENTION: HERATITIS C VIRUS INFECTION

7 TITLE OF INVENTION HERATITIS C VIRUS INFECTION

7 TITLE OF INVENTION NUMBER: US/09/504,231A

7 TITLE OF INVENTION NUMBER: 09/274,553

PRIOR PELLICATION NUMBER: 09/257,608

PRIOR PELLICATION NUMBER: 60/109,12

7 PRIOR PELLICATION NUMBER: 60/100,842

PRIOR PELLICATION NUMBER: 60/100,842

PRIOR PELLING DATE: 1999-02-24

PRIOR PELLING DATE: 1999-04-27

8 NUMBER OF SEQ ID NOS: 3242

8 SOFTHARE: Patentin version 3.0

8 SEQ ID NO 1178

LENGTH: 15
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Sequence 1179, Application US/09504231A

Patent No. US20020013488A1

GENERAL INPORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Beth

APPLICANT: Roberts, Dennis

TITLE OF INVENTION: HEAPATITIS C VIRUS INFECTION

TITLE OF INVENTION: HEAPATITIS C VIRUS INFECTION

FILE REFERENCE: rpi 247/282

CURRENT APPLICATION NUMBER: US/09/504,231A

CURRENT APPLICATION NUMBER: US/09/504,231A

FILE REPERING DATE: 1999-03-23

PRIOR PILING DATE: 1999-03-23

PRIOR PILING DATE: 1999-02-24

PRIOR PLING DATE: 1999-02-24
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US-09-504-231A-1178
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14.3%; Score 11; DB
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches
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PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
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     11; Conservative
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                                                              43 AGGTAAAGAGC
     Matches
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| Sequence 20, Application US20030188326A1
| Sequence 20, Application No. US20030188326A1
| GENERAL INFORMATION:
| APPLICAMY: D'Andrea Alan
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILI:
| TITLE OF INVENTION: DEPECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
| FILE REFERENCE: 7032/2055
| CURRENT FILING DATE: 2002-06-06
| PRIOR PLLICATION NUMBER: US 60/998,027
| PRIOR PLLING DATE: 2001-11-02
| PRIOR PLLING DATE: 2001-11-03
| PRIOR FILING DATE: 2001-11-03
| PRIOR FILING DATE: 2001-11-03
| WUMBER OF SEQ ID NOS: 352
| SOUTHARE: Patentin version 3.1
| SEQ ID NO 20
| LENTH: 14
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US-09-998-027-20
1S-09-998-027-20
Sequence 20, Application US/0998027
Publication No. US20030093819A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: DNA Repair Mechanisms
CURRENT APPLICATION NUMBER: US/09/998,027
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 14
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                                                                                                                                           ; OTHER INFORMATION: Oligonucleotide for detection of SNP ISC0054826
US-10-257-017B-224918
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14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 11; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Intron/Exon Junctions of FANCD
US-09-998-027-20
                                                                                                                                                                                                                              Score 11; DB 1;
Pred. No. 48;
                                                                                                                                                                                                                              Query Match 14.3%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 48; Matches 11; Conservative 0; Mismatches
                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
US-10-165-099-20
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ORGANISM: Homo sapien
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Best Local Similarity
SEQ ID NO 224918
LENGTH: 13
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TYPE: RNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1179
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Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels
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Job time : 0.001 secs
                      PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR PILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3148
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1179
LENGTH: 15
  PRIOR APPLICATION NUMBER: 09/257,608
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APPLICANT: Blatt, Lawrence
APPLICANT: Blatt, Lawrence
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Rocejak, Dennis
TITLE OF INVENTION: BRIXWATIC WICKEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
FILE REPERBUGE: rpi 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
FRIOR PILING DATE: 1999-02-24
PRIOR APPLICATION WUMBER: 60/100,842
PRIOR PILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-04-27
WUMBER: PAPLICATION WUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
SOFTWARE: PATENTH IN VERSION 3.0
SEQ ID NO 1178
LENGTH: 15
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US-09-274-553D-1179/c
US-09-274-553D-1179/c
Sequence 1179, Application US/09274553D
Facent No. US20020062225A1
GENERAL INFORMATION:
APPLICANT: Blatt, Lawrence
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Roberts, Beth
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: HERATITE C VIRUS INFECTION
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mucleic Acid Target
US-09-504-231A-1179
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US-09-274-553D-1178
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US-09-274-553D-1178/c
; Sequence 1178, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
SOFTWARE: Patentin version 3.0
SEQ ID NO 1179
LENGTH: 15
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ORGANISM: Artificial Sequence
                                                                               TYPE: RNA
ORGANISM: Artificial Sequence
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US-10-310-914A-562241

US-11-101-244-197126

US-11-101-244-518286

US-11-101-244-518286

US-11-101-244-518284

US-11-101-244-518284

US-11-101-244-518284

US-11-101-244-618922

US-11-101-244-749629

US-11-101-244-19751

US-11-101-244-19751

US-11-101-244-106983

US-11-101-244-1138798

US-11-083-784-118286

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US-11-083-784-518286

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                                      US-11-101-244-741998

US-11-101-244-1221841

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US-11-083-784-462186

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Sequence 972474, Sequence 1012488, Sequence 1034219, Sequence 1036393, Sequence 1155168, Sequence 1125172, Sequence 1127400, Sequence 1127400, Sequence 1127430, Sequence 1127430, Sequence 1127430, Sequence 1151972, Sequence 1151972, Sequence 1159676, Sequence 1159676,	Sequence 1492356, Sequence 1512594, Sequence 1512594, Sequence 150055, Sequence 1570062, Sequence 1570074, Sequence 1570074, Sequence 24159, A Sequence 24159, A Sequence 24159, A Sequence 24159, Sequence 2195690, Sequence 219414, Sequence 276236, Sequence 276236, Sequence 387184, Sequence 387184,	Sequence 3187492, Sequence 410730, Sequence 410029, Sequence 5112370, Sequence 512370, Sequence 529822, Sequence 550822, Sequence 560822, Sequence 624448, Sequence 680973, Sequence 710507, Sequence 710507, Sequence 710507, Sequence 785114, Sequence 785140,	Sequence 972375, Sequence 972375, Sequence 1012488, Sequence 1012488, Sequence 1155168, Sequence 1249609, Sequence 1227400, Sequence 1327400, Sequence 1359582, Sequence 1359582, Sequence 1418701, Sequence 149255, Sequence 149256, Sequence 149256, Sequence 149256, Sequence 1512594, Sequence 1512594, Sequence 1512597,
			US-11-083-784-972375 US-11-083-784-972375 US-11-083-784-1012488 US-11-083-784-1036393 US-11-083-784-1036393 US-11-083-784-1036393 US-11-083-784-1155168 US-11-083-784-1245609 US-11-083-784-1327400 US-11-083-784-1359582 US-11-083-784-1359582 US-11-083-784-1418701 US-11-083-784-1418701 US-11-083-784-1492356 US-11-083-784-1492356 US-11-083-784-1492356 US-11-083-784-1512594 US-11-083-784-1512594 US-11-083-784-1512594 US-11-083-784-1512594
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US-11-101-244-1197318

Sequence 1197318, Application US/11101244

Sequence 1197318, Application US/11101244

Sequence 1197318, Application US/11101244

GENERAL INFORMATION:
APPLICANT: Darmacon, Inc.
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF ERQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1197318
LENGTH: 19
                                                                                                                                                                                                                                DB 1; Length 19;
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US-11-01-244-1197383
Sequence 1197383, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Charmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Searinge, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILLE REPRESENCE: 13499US
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Pred. No. 57;
0; Mismatches
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 512380
LENGTH: 19
                                                                                                                                                                                                                                                                                                                        23 CAACTCTGGAGTCCTCTGA 41
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Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                      TYPE: RNA
CONGANISM: Homo sapiens
US-11-083-784-512380
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CORGANISM: Homo sapiens
US-11-101-244-1197318
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Daramacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Responds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Benerall, William

APPLICANT: Boarings, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFRERENCE: 1349908

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR FILING DATE: 2003-11-16

PRIOR FILING DATE: 2003-10-10
                       NUMBER OF SEQ ID NOS: 673904
SOCTIFIARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 18534
LENGTH: 25
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
PILE REPERENCE: 13499US
                                                                                                                                                                                                         11 Score 17.6; I ilarity 83.3%; Pred. No. 41; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 512380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17.4;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-101-244-512380/c; Sequence 512380, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     29 TGGAGTCCTCTGAGAGGTAAAGAG 52
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    PRIOR FILING DATE: 2004-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-512380
                                                                                                                                      ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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Best Local Similarity
Matches 20; Conserv
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US-11-083-784-512380/c
                                                                                                                                                                US-11-121-849-18534
                                                                                                                      TYPE: DNA
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| Publication No. USGO050245475A1 |
| GENERAL INFORMATION: |
| APPLICANT: BANDORA, Ansstasia | APPLICANT: Revnoids, Ansstasia | APPLICANT: Revnoids, Ansstasia | APPLICANT: Beake, Devin |
| APPLICANT: Beake, Devin | APPLICANT: Beake, Devin |
| APPLICANT: Scaringe, Stephen | TITLE OP INVENTION: Functional and Hyperfunctional siRNA |
| PLICE OF INVENTION: Punctional and Hyperfunctional siRNA |
| TITLE OP INVENTION: Punctional and Hyperfunctional siRNA |
| PRICE REPREMENT 2003-03-18 |
| PRICE PLICATION NUMBER: US/10/714,333 |
| PRICE PLICATION NUMBER: 60/502,050 |
| PRICE PLICATION NUMBER: 60/502,050 |
| PRICE PLICATION NUMBER: 60/426,137 |
| PRICE PLICATION NUMBER: 60/426,137 |
| NUMBER: OF SEQ ID NOS: 1591911 |
| SOFTWARE: Proprietary |
| SEQ ID NO 1197318 |
| LENGTH: 19
                                                                                                                                                                                                                         DB 1; Length 19;
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynoids, Angela
APPLICANT: Reynoids, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANTON Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR PILING DATE: 2003-11-14
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                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                         Score 16.4;
Pred. No. 75
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                                                                                                                                                                                                                                                                                                                   58 GAAGCTGATGTCCTGTCA 75
                                                                                                                                                                                                                                                                                                                                                    ||||||:| :|:||:||:|| GAAGCUGUGUCA 19
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66.7%;
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21.3%;
Best Local Similarity 66.7%;
Matches 12; Conservative
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1197383
                                                                                                                                                                                                                       Query Match 21.3
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                        TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1197383
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US-11-083-784-1197318
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Sequence 99908, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biler, Kvuzat
TITLE OF INVERTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
TITLE OF INVERTION: 10087.0200.CPUS01
GURRENT PAPLICANTION NUMBER: 105/10/310,914A
CURRENT PLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 99908
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1373610/c
Sequence 1373610, Application US/10310914A
Sequence 1373610, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses 101/10/310, 914A
CURRENT PELLING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1373610
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Pred. No. 75;
5; Mismatches 1; Indels
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Pred. No. 65;
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Pred. No. 72;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOOTWARE: Proprietary
SEQ ID NO 1197383
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                       S8 GAAGCTGATGTCCTGTCA 75
                                                                                                                                                                                                                                                                                                                                                            27 TCTGGAGTCCTCTGAGAG 44
                                                                                                                                                                                                                                                     21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.3%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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il Similarity 85.7%;
18; Conservative
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Best Local Similarity 66.7
Matches 12, Conservative
                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-11-083-784-1197383
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Best Local Similarity
Matches 18; Conserv
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US-10-310-914A-99908/c
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Sequence 3819, Application US/11069908
Publication No. US20050266432A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLIPHANT, ARNOLD
APPLICANT: OLIPHANT, ARNOLD
APPLICANT: OLIPHANT, ARNOLD
APPLICANT: OLIPHANT, SARAH
TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
TITLE OF INVENTION: 029011-0402
CURRENT APPLICATION NUMBER: US/11/069,908
FILE REFERENCE: 029011-0402
CURRENT APPLICATION NUMBER: 60/547,823
FRIOR FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 7098
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 3819
ILENGTH: 22
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US-10-310-914A-1094322/c

Sequence 1094322, Application US/10310914A

Sequence 1094322, Application US/10310914A

Publication No. US2060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Baniler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
                                                       APPLICANT: FARTI, DEMIS
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INPERRING CANINE BREEDS
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INPERRING PARENTAGE OF CANINE ANIMALS
FILE REFERENCE: MMI1120-4
CURRENT PEDLICATION NUMBER: US/10/972,767
CURRENT PEDLICATION NUMBER: US 60/617,383
PRIOR FILING DATE: 2004-10-25
PRIOR FILING DATE: 2004-10-24
NUMBER OF SEQ ID NOS: 404
SOFTWARE: PATENTION NUMBER: 105 60/514,180
NUMBER OF SEQ ID NOS: 404
SOFTWARE: PATENTION NUMBER: 203-10-24
NUMBER OF SEQ ID NOS: 404
SOFTWARE: PATENTION VERSION 3.3
LENGTH: 21
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-3819
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20.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 89.5%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Amplification Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 TGAGAGGTAAAGAGCCAGC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGAGTGGTAATAGCCAGC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial sequence
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DeNise, Sue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-069-908-3819/c
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                                                                                                                                                                                                                                             Sequence 50127, Application US/10310914A
| Publication No. US20060003322A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Kvuzat
| TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
| TITLE OF INVENTION: uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 201349, Application US/10310914A
| Publication No. US20060003322A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Kvuzat
| APPLICANT: Bentwich, Kvuzat
| TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
| TITLE OF INVENTION: uses thereof
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76.2%; Pred. No. 65;
:ive 2; Mismatches
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76.2%; Pred. No. 65;
:ive 2; Mismatches
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Publication No. US20060008815A1
GENERAL INFORMATION:
APPLICANT: METAMORPHIX, INC.
APPLICANT: Rosenfeld, David
APPLICANT: Refr. Richard
APPLICANT: Hutton, Michelle
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                                  31 GAGTCCTCTGAGAGGTAAAGA 51
                                                                                            21 GAGTCTTCTGAGGGCTAAGGA 1
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Best Local Similarity 76.2%
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Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                RESULT 11
US-10-310-914A-591217
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US-10-310-914A-921349
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US-10-972-767-181
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TYPE: RNA
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US-11-101-244-826612/C

Sequence 826612, Application US/11101244

Publication No. US20550246794A1

GENERAL INFORMATION:
APPLICANT: Diarmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Scaringe, Stephen
ITLE REPRENCE: 13499US
CURRENT PILIANG DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR PILING DATE: 2003-09-10
FRIOR PILING DATE: 2003-01-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary
SEQ ID NOS: 1591911

SEQ ID NO 826612
                                                                                                                                                                                                                                                          DB 1; Length 22;
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Drawcon, Inc.
APPLICANT: Reymolds, Angela
APPLICANT: Reymolds, Angela
APPLICANT: Rezmolds, Angela
APPLICANT: Rezmolds, Angela
APPLICANT: Rezmolds, Angela
APPLICANT: Rezmolds, Angela
APPLICANT: Marahall, William
APPLICANT: Marahall, William
APPLICANT: Boaringe, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07

PRIOR PLING DATE: 2003-09-10
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Best Local Similarity 81.8%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches
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PILE REFERENCE: 06087.0200.CPUS01
CURRENT PEPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn Version 3.3
SEQ ID NO 1994322
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                   11 GGCCTGGGGATACAACTCTGGA 32
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ORGANISM: Homo gapiens
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Best Local Similarity
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Best Local Similarity
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ORGANISM: Human
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Pred. No. 98;
5; Mismatches 1; Indels
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; Publication No. US20050246794A1
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; APPLICANT: Marchall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; PILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2002-11-14
; SOFTHARE: PEPPLICATION NUMBER: 60/426,137
; ROTHARE: PEPPLICATION NUMBER: 50/426,137
; SOFTHARE: PEPPLICATION
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; SOFTHARE: PEPPLICATION
; SEQ ID NO 1197395
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Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dhrancon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Marchall, Millam

APPLICANT: Marchall, William

APPLICANT: Marchall, William

TITLE OF INVENTION: Functional and Hyperfunctional sirNA

FILE OF INVENTION: Punctional and Hyperfunctional sirNA

FILE REFERENCE: 13499US

CURRENT FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PLING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 60/426,137
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Pred. No. 98;
5; Mismatches
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1197334
LENGTH: 19
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Best Local Similarity 64.7%;
Matches 11; Conservative
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Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1197334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dharmacon, Inc.
APPLICANT: Character, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Respondes, Angela
APPLICANT: Respondes, Angela
APPLICANT: Scaringe, Stephen
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILER REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PRILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1197395
LENGTH: 19
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Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: DAWAROON, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

PILE REPERRUCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784
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                   PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION UNMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1197334
LERIGTH: 19
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Best Local Similarity 64.7%;
Matches 11; Conservative
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US-11-083-784-1197395
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Matches 11; Conserv
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US-11-083-784-1375618
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                                                                                                                                                                                             TYPE: RNA
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US-11-083-784-826612/c
| Sequence 826612, Application US/11083784
| Publication No. US20050245475A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Leake, Devin
| APPLICANT: Leake, Devin
| APPLICANT: Leake, Devin
| APPLICANT: Leake, Devin
| APPLICANT: Laske, Devin
| APPLICANT: All 14 William
| APPLICANT: Laske, Devin
| APPLICANT: All 14 William
| APPLICANT: Laske, Devin
| PRIOR PLING DATE: 2005-03-18 PRIOR APPLICATION NUMBER: 60/502,050 PRIOR APPLICATION NUMBER: 60/502,050 PRIOR APPLICATION NUMBER: 60/426,137 PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2003-09-10 PRIOR FILING DATE: 2003-09-10 PRIOR FILING DATE: 2003-11-14 NUMBER OF SEQ ID NOS: 1591911 SOFTWARE: Proprietary
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| Publication No. US20050245475A1
| GENERAL INFORMATION:
| APPLICANT: Dearmacon, Inc.
| APPLICANT: Revnolds, Angela
| APPLICANT: Revnolds, Angela
| APPLICANT: Leake, Devin
| APPLICANT: Leake, Devin
| APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
| TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
| FILE REFERENCE: 13499US
| CURRENT FILING DATE: 2005-03-18
| PRIOR PILING DATE: 2003-11-14
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64.7%; Pred. No. 98;
tive 5; Mismatches
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
                                                                                                                                                                                                                                       Best Local Similarity 64.7
Matches 11; Conservative
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    ORGANISM: Homo sapiens
US-11-101-244-1375618
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US-11-083-784-826612
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Best Local Similarity
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US-11-083-784-1197334
                                                                     SEQ ID NO 1375618
LENGTH: 19
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US-10-310-914A-946704/C
US-10-310-914A-946704/C
US-10-310-914A-946704/C
Sequence 946704, Application US/10310914A
Publication No. US2006000332A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Kwuzat
APPLICANT: Shiler, Kwuzat
APPLICANTON: Uses thereof
TITLE OF INVENTION: Uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1213419
| Sequence 1213419 | Application US/10310914A |
| Sequence 1213419, Application US/10310914A |
| Sequence 1213419, Application US/10310914A |
| Publication No. US2006000332A1 |
| Publication No. US2006000332A1 |
| APPLICANT: Bentwich: Kvuzat |
| APPLICANT: Bentwich: Kvuzat |
| APPLICANT: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof |
| TITLE OF INVENTION: uses thereof |
| TITLE OF INVENTION: US/10.010 |
| TITLE OF INVENTION: US/10.010 |
| TITLE REFERENCE: 06087,0200.CPUS01 |
| CURRENT APPLICATION WUMBER: US/10/310,914A |
| CURRENT FILING DATE: 2002-12-06 |
| NUMBER OF SEQ ID NOS: 1388402 |
| SOFTWARE: PatentIn version 3.3 |
| SEQ ID NO 1213419 |
| LENGTH: 18 |
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        DB 1; Length 20;
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66.7%; Pred. No. 1.18+02;
ive 5; Mismatches 0; Indels
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; Score 15.2; Di
; Pred. No. 98;
0; Mismatches
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Pred. No. 93;
0; Mismatches
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                                                                                                                    42 GAGGTAAAGAGCCAGCGAAG 61
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/ Match 19.7%;
Local Similarity 85.0%;
Les 17; Conservative (
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85.0%;
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Best Local Similarity 66.77
Matches 10; Conservative
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Best Local Similarity 85.0
Matches 17; Conservative
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US-10-310-914A-946704
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        Query Match
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Sequence 820857, Application US/10310914A

Sequence 820857, Application US/10310914A

Publication No. US20060003322A1

Sequence 820857, Application US/10310914A

Publication No. US2006000332A1

APPLICANT: Bailer, Kvuzat

APPLICANT: Bailer, Kvuzat

APPLICANT: Bailer, Kvuzat

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION UNMERE: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 820857

LENGTH: 20
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SEQ ID NO 173632
LENGTHRE: Patentin version 3.3
SEQ ID NO 173632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
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; Sequence 1373632, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Issac
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                                                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1375618
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Best Local Similarity
Matches 11; Conserva
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Best Local Similarity
Matches 16; Conserva
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; ORGANISM: Human
US-10-310-914A-820857
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APPLICANT: Bentwich, Isaac

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Sequence 1358783, Application US/10310914A

Subjication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biller, Kvuzat
TITLE OF INVENTION: uses thereof
FILE REFRENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1358783
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 446294, Application US/11101244
publication No. US200S0246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Resynolds, Angela
APPLICANT: Ascaringe, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-010
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 446294
LENGTH: 19
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tive 0; Mismatches 2;
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US-11-101-244-446294
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US-10-310-914A-1358783/c
                                                                                                                                                           Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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US-11-101-244-446294/c
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pubnew.

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 45021
LENGTH: 18
TYPE: LENGTH: 18
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses through
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: Patentin version 3.3
SEQ ID NO 921346
LENGTH: 18
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Publication No. US20060003322A1
RUBLICATION.
SEQUENCE NO. US20060003322A1
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Women With Soft Solor CPUSO1
CURRENT PLIEM REFERENCE: 06097.0200.CPUSO1
CURRENT PLIEMS DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 946718
LENGTH: 18
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US-10-310-914A-921346
; Sequence 921346, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORWATION:
; APPLICANT: Bentwich, ISBBC
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Matches 14; Conserv
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Best Local Similarity
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US-10-310-914A-946718/c
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US-10-310-914A-946718
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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; ORGANISM: Homo sapiens
US-11-101-244-686604
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US-11-101-244-716743
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US-11-101-244-716743/c
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Sequence 462186, Application US/11101244

| Sequence 462186, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Revnoids, Anastasia
| APPLICANT: Revnoids, Angela
| APPLICANT: Revnoids, Angela
| APPLICANT: Revnoids, Angela
| APPLICANT: Beake, Devin
| PRICANT: BERERRENCE: 13499US
| CURRENT PILING DATE: 2005-04-07
| PRIOR PILING DATE: 2005-04-07
| PRIOR PILING DATE: 2003-09-10
| PRIOR PILING DATE: 2002-11-14
| WUMBER: Proprietary
| SEQ ID NO 462186
| LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.2%; Score 14.8; DB 1; Length 19; 66.7%; Pred. No. 1.1e+02; tive 4; Mismatches 2; Indels
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.;
APPLICANT: Reynolds, Angela
APPLICANT: Beake, Devin
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
FROMENT: PROPRIETARY
FROMENT: PROPRIETARY
SEQ ID NOS: 1591911
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Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-462186
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ORGANISM: Homo sapiens
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US-11-101-244-673763
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Sequence 686604, Sphication Us/1101244

Sequence 686604, Sphication Us/1101244

Sequence The Marker Construction of the Marker Co
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RESULT 37 US-11-101-244-741998

RESULT 35

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Sequence 446294, Application US/11083784
Publication No. US20050245475A1
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  Publication No. US20050246794A1
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1221940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1222038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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US-11-083-784-446294/C
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US-11-101-244-1222038
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                                                           APPLICANT: Characon, Inc.
APPLICANT: Characon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Searinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPRIETERY
SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Khronova, Anastasia
APPLICANT: Khronova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENITON: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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US-11-101-244-1221940
; Sequence 1221940, Application US/11101244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1221841, Application US/11101244; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
Sequence 741998, Application US/11101244
Publication No. US20050246794A1
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Best Local Similarity 66.7
Matches 12; Conservative
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US-11-101-244-741998
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US-11-101-244-1221841
                          Publication No. US20(
GENERAL INFORMATION:
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LENGTH: 19
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 1222038, Application US/11101244
| Carguence 1222038, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INPORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Merball, Walliam
| APPLICANT: Marball, Walliam
| PREBRECANT: Functional and Hyperfunctional siRNA
| FILE REFERENCE: 13499US
| CURRENT APPLICATION NUMBER: 60/407
| PRIOR APPLICATION NUMBER: 60/426,137
| PRIOR FILING DATE: 2003-01-14
| NUMBER OF SEQ ID NOS: 1591911
| SEQ ID NO 1222038
| LENGTH: 19
GENERAL INFORMATION:
APPLICANT: CANTON:
APPLICANT: Reynolds, Anselas
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1221940
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US-11-083-784-686604
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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         APPLICANT: Reviolds, Angela
APPLICANT: Reviolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
FILE REPRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2003-018
PRIOR PILING DATE: 2003-019
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FULLIALLY COURER OF THE PERERENES: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER: OF SEQ ID NOS: 1591911
SEQ ID NO 462186
LENGTH: 19
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Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
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Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-446294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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RESULT 43

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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66604, Application US/11083784
; Sequence 66604, Application US/11083784
; Publication No. US20050245475A1
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Characon, Inc.;
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Marball, William
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Scaringe, Stephen
; TILE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499U
; CURRENT APPLICATION NUMBER: US/11/043,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR PLLICATION NUMBER: 60/502,050
; PRIOR PLLING DATE: 2003-19-14
; RIOR PLLING DATE: 2003-19-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 68604
; LENGTH: 19
                                         GENERAL INFORMATION: 0200243347341

APPLICANT: Dharmacon, Inc.
APPLICANT: RAyorous, Ansatasia
APPLICANT: RAyorous, Ansatasia
APPLICANT: Reynolds, Angela
APPLICANT: Respondes, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PLILING DATE: 2003-10-10
PRIOR PLILING DATE: 2003-11-14
SPRIOR PLILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
IENGTH: 19
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Sequence 673763, Application US/11083784
Publication No. US20050245475A1
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US-11-083-784-673763
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; ORGANISM: Homo sapiens
US-11-083-784-686604
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Best Local Similarity
Matches 15; Conserva
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42 GAGGTAAAGAGCCAGCGA 59
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Best Local Similarity 66.7%;
Matches 12; Conservative
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US-11-083-784-1221841
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US-11-083-784-1221940
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                                                                                                           US-11-083-784-716743/C

| Sequence 716743, Application US/11083784
| Sequence 716743, Application US/11083784
| GENERAL INFORMATION OF US2005024547541
| GENERAL INFORMATION | Inc.
| APPLICANT: BATOONA, Anastasia | APPLICANT: Reynolds, Angela | APPLICANT: Reynolds, Angela | APPLICANT: Reynolds, Angela | APPLICANT: Leake, Devin | APPLICANT: Scaringe, Stephen | TITLE OF INVENTION: Munchional and Hyperfunctional siRNA | TILE REFERENCE: 13499US | US/11/083,784 | CURRENT APPLICATION NUMBER: US/11/083,784 | CURRENT PILLING DATE: 2005-03-18 | PRIOR APPLICATION NUMBER: 60/502,050 | PRIOR PILLING DATE: 2003-11-14 | PRIOR APPLICATION NUMBER: 60/502,050 | PRIOR PILLING DATE: 2003-09-10 | PRIOR APPLICATION NUMBER: 60/426,137 | PRIOR APPLICATION NUMBER: 60/426,13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 1; Length 19;
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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US-11-083-784-741998
; Sequence 741998, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Charmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILIATE DATE: 2005-03-18
PRIOR PILIATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
SOFTWARE: PROPRIET : 1591911
SOFTWARE: PROPRIET : 1591911
LENGTH: 19
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Best Local Similarity 88.9%;
Matches 16; Conservative
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US-11-083-784-741998
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US-11-083-784-716743
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Sequence 1221841, Application US/11083784
; Sequence 1221841, Application US/11083784
; Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Actinge, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional giRNA;
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: 005-03-18
FRIOR PLILING DATE: 2003-01-10
FRIOR PLILING DATE: 2003-01-10
FRIOR PLILING DATE: 2003-01-10
FRIOR PLILING DATE: 2003-01-10
FRIOR PLILING DATE: 2003-11-14
FRIOR PLILING DATE: 2002-11-14
SPRIOR PLILING DATE: 2002-11-14
SOFTWARE: Proprietary
SEQ ID NO 1221841
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 1; Length 19;
Pred. No. 1.1e+02;
4; Mismatches 2; Indels
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Sequence 1221940, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Edwing Marginal

APPLICANT: Reynolds, Angela

APPLICANT: Marball, William

APPLICANT: Marball, William

APPLICANT: Marball, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

TILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR PLILOATION NUMBER: 60/502,050

PRIOR PLILOATION NUMBER: 60/502,050

PRIOR PLILOATION NUMBER: 60/426,137

PRIOR PLILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1221940

LENGTH: 19

LENGTH: 19
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Sequence 144915, Application US/10310914A
Publication No. US20060003322A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: Patentin version 3.3
SEQ ID NO 144915
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US-11-101-244-527885/C
Sequence 527885, Application US/11101244
Fublication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Diarmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Beanning, Angela
APPLICANT: Scarings, Stephen
APPLICANT: Barings, Stephen
APPLICANT: Branchil, William
APPLICANT: Murshill, William
APPLICANT: APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE PEOPLICATY
SEQ ID NO 527885
LENGTH: DATE: DATE: THE PEOPLICATY
TYDE: DATE: DATE: THE PEOPLICATY
TYDE DATE: THE PEOPLICATY
THE PEOPLICATY
THE PEOPLICATY
THE PEOPLICATION NUMBER: Of 426, 137
PRIOR FILING DATE: 2002-11-14
TYDE: DATE: PEOPLICATY
THE PEOPLICATY
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Pred. No. 1.3e+02;
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18.7%; Score 14.4; DB 1;
Best Local Similarity 93.8%; Pred. No. 1.38+02;
Matches 15; Conservative 0; Mismatches 1;
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; Sequence 681299, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION;
; APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ACAAGACGGCCTGGGG 19
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Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 53
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TITLE OF INVENTION: Baloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1045625
LERNGTH: 20
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                                                                                                                                                                                                                                                                      Sequence 1222038

Sequence 1222038, Application US/11083784

Sequence 1222038, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Revoca, Anastasia

APPLICANT: Revoca, Anastasia

APPLICANT: Revocalds, Anastasia

APPLICANT: Revocalds, Anastasia

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE REFERENCE: 1349908

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT PILING DATE: 2005-03-18

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1222038

LENGTH: 19
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                                  2; Indels
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2
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1 CAGAGAAGCUGCUGUCCU 18
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Best Local Similarity 66.7v
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Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i TYPE: RNAj ORGANISM: Homo sapiensUS-11-083-784-1222038
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
SOFTWARE: Proprietary
SEQ ID NO 1155118
LENGTH: 19
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Fublication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Revaco, Anastasia
APPLICANT: Revaco, Angela
APPLICANT: Revaco, Povin
APPLICANT: Revacols, Angela
APPLICANT: Marball, William
APPLICANT: NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ACAACTCTGGAGTCCT 37
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Best Local Similarity 93.8°
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1155118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Homo sapiens
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US-11-101-244-1025484/C

Sequence 1025484, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION NO. US20050246794A1

APPLICANT: Branacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Carninge, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

PRICARENT SCATION NUMBER: US/11/101,244

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1025484

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APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13490US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PPLICATION NUMBER: 60/502,050
PRIOR PPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 20003-09-10
PRIOR PLING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 681299
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ORGANISM: Homo sapiens
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US-11-101-244-1025484
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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US-11-101-244-1155118
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Query Match 18.7%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 1.3e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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; Publication No. US20050246794A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reyanolds, Angela
APPLICANT: Reyanolds, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT PILING DATE: 2005-06.07
PRIOR PPLICATION NUMBER: 60/426,137
PRIOR PPLICATION NUMBER: 60/426,137
PRIOR PPLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 2002-11-14
SOFTWARE: PEPPLICATION
SEQ ID NOS: 1591911
SENGID NO 1526053
LENGTH: 19
  APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional sirna
FILE REFERENCE: 1349908
CURRENT PAPLICATION NUMBER: US/11/101,244
CURRENT PAPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTHANE: 19
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; Sequence 527885, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
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Best Local Similarity 93.8
Matches 15; Conservative
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ORGANISM: Homo sapiens
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US-11-101-244-1526053
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i Sequence 1435551, Application US/11101244

i Publication No. US20050246794A1

i GENERAL INFORMATION:

i APPLICANT: Revolva, Anastasia

APPLICANT: Revolva, Anastasia

APPLICANT: Revolda, Anastasia

APPLICANT: Revolda, Anastasia

APPLICANT: Revolda, Anastasia

APPLICANT: Revolva, Mastasia

APPLICANT: Leake, Devin

i APPLICANT: Scaringe, Stephen

i TILLE OF INVENTION: Functional and Hyperfunctional sirna

PILLE OF INVENTION: Punctional and Hyperfunctional sirna

PILLE OF INVENTION NUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR FILING DATE: 2005-09-10

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1435551

LENGTH: 19
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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE AND SCARINGE, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 08/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1323244
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| Sequence 1526025, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: KIVOCOVA, Anastasia
| APPLICANT: RYDOCOVA, Anastasia
| APPLICANT: Leake, Devin
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Matches 11; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-143551
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18.7%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 1.3e+02; Live 0; Mismatches 1; Indel8
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APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional SIRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LEMOTH: 19
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                                      APPLICANT: Neglacia, Augusta, Applicant: Applicant: Leake, Devin APPLICANT: Marshall, William APPLICANT: Scaringe, Stephen String Daring, Stephen String Daring, Stephen String Daring, Stephen String Daring Daring
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; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
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           Reynolds, Angela
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US-11-083-784-1025484
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US-11-083-784-1256070/c
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US-11-083-784-1155118
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## APPLICANT: Scaringe, Stephen
## TITLE OF INVENTION: Functional and Hyperfunctional sirna
## FILE REFREENCE: 13499US
## CURRENT APPLICATION NUMBER: US/11/083,784
## CURRENT PILING DATE: 2005-03-18
## PRIOR APPLICATION NUMBER: US/10/714,333
## PRIOR PILING DATE: 2003-11-14
## PRIOR PILING DATE: 2003-11-14
## PRIOR PILING DATE: 2003-09-10
## PRIOR PILING DATE: 2003-09-10
## PRIOR PILING DATE: 2003-09-10
## RIOR PILING DATE: 2003-09-11
## NUMBER OF SEQ ID NOS: 1591911
## NUMBER OF SEQ ID NOS: 1591911
## SEQ ID NO $27885
## LENGTH: 19
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APPLICANT: KNOTOVA, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
FRIOR RILING DATE: 2005-03-18
PRIOR PLILMG DATE: 2003-11-14
PRIOR PLILMG DATE: 2003-10-10
PRIOR PLILMG DATE: 2003-09-10
PRIOR PLILNG DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
IENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 681299, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Charmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 GAAGCTGATGTCCTGT 73
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Best Local Similarity 75.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-083-784-527885
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; ORGANISM: Homo sapiens
US-11-083-784-681299
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US-11-083-784-1025484/c
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US-11-083-784-681299
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US-11-083-784-1526025/C

is Sequence 1526025, Application US/11083784

j Publication No. US-20050245475A1

GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2002-11-14

NUMBER: OF SEQUENCE: PROPRIET ON NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14

SEQ ID NO 1526025

LENGTHER PORTION NUMBER: SOUTH APPLICATION APPLICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.7%; Score 14.4; DB 1; Length 19; Best Local Similarity 93.8%; Pred. No. 1.3e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                               GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Enhormed, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Acaring, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 143551
LEMOTTH: 19
Sequence 1435551, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
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US-11-083-784-1435551
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US-11-083-784-1526025
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; Sequence 1323344, Application US/11083784
; GENERAL INFORMATION
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OP INVENTION: Punctional and Hyperfunctional sirna
; APPLICANT: Scaringe, Stephen
; TITLE OP INVENTION: Punctional and Hyperfunctional sirna
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR PILING DATE: 2003-10-10
; PRIOR PILING DATE: 2003-11-14
; PRIOR PILING DATE: 2003-11-14
; PRIOR PILING DATE: 2002-11-14
; PRIOR PILING DATE: 2002-11-14
; PRIOR PILING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NO 132344
; LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.7%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
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                       APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Purctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: G6/502,050
PRIOR APPLICATION NUMBER: 66/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PLILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 68.8
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-1256070
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US-11-083-784-1323244
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RESULT 67

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Sequence 562241, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 562241
LENGTH: 19
                                                                                                                                  Sequence 15591, Application US/10750623

Sequence 15591, Application US/10750623

Publication No. US20050297531A1

GENERAL INFORMATION:

APPLICANT: WMI GENOMICS, INC.

APPLICANT: BONISE, Sue K.

APPLICANT: ROSENPELD, David

APPLICANT: BATES, Stephen

APPLICANT: PATINO, IMPRIPOS AND SYSTEMS FOR INPERRING BOVINE TRAITS

TITLE OF INVENTYION: METHODS AND SYSTEMS FOR INPERRING BOVINE TRAITS

TITLE OF INVENTYION: METHODS AND SYSTEMS FOR INPERRING BOVINE TRAITS

FILE REFERENCE: WMILLOG-1

CURRENT APPLICATION NUMBER: US 60/437,482

FRIOR PILLING DATE: 2003-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE PATENTY OF SEQ ID NOS: 64922

SEQ ID NO 15591

LENGTH: 20
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Pred. No. 1.38+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 18.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
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US-10-310-914A-1111642/c
; Sequence 1111642, Application US/10310914A
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence
20 AACTCTGGAGTCGTCT
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US-10-310-914A-562241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-750-623-15591
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Sequence 15591, Application US/10750185

Publication No. US2000260603A1

GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ADMIN' Tom
APPLICANT: PANTIN' Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TILLE REFERENCE: MMI1100-12-31
FILLE REFERENCE: MMI100-12-31
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin Version 3.1
LENGTH: 20
LENGTH: 20
LENGTH: 20
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                    APPLICANT: Khyozova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marehall, William
APPLICANT: Marehall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional sirNa
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2003-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 06/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
SPRIOR PILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 1591911
                                                                                                    ; Sequence 1526053, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Forward Primer US-10-750-185-15591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.7%;
93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTGGAGTACTCTGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.7
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                    APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-083-784-1526053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1526053
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24 AACTCTGGAGTCCTCT 39

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 518286, Application US/11101244
; Sequence 518286, Application US/11101244
; Publication No. U3202050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Easke, Devin
; APPLICANT: Reynolds, Angela
; APPLICANT: Marchall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/520,050
; PRIOR PLICATION NUMBER: 60/426,137
; PRIOR PLICATION NUMBER: 60/426,137
; PRIOR PLICATION NUMBER: 60/426,137
; SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NOS: 1591911
     ; TITLE OF INVENTION: Functional and Hyperfunctional sirNA; FILE REFERENCE: 13499US; CURRENT PEPLICATION NUMBER: US/11/101,244; CURRENT FILING DATE: 2005-04-07; PRIOR APPLICATION NUMBER: 60/502,050; PRIOR PILING DATE: 2003-09-10; PRIOR PILING DATE: 2003-09-10; PRIOR PILING DATE: 2003-09-10; PRIOR PILING DATE: 2002-11-14; NUMBER OF SEQ ID NOS: 1591911; SSCHWARE: PROPIECTERY; SEQ ID NOS: 1591911; SSCHWARE: PROPIECTERY
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APPLICANT: Exproson, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
IITLE OF INVENTION: Punctional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
18.4%; Score 14.2; DB 1;
Best Local Similarity 84.2%; Pred. No. 1.38+02;
Matches 16; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 GGATACAACTCTGGAGTCC 36
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ORGANISM: Homo sapiens
US-11-101-244-518286
                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-101-244-404601
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US-11-101-244-527824/c
                                                                                                                                                                                                                                                                                                                   TYPE: RNA
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Sentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFREENCE: 60697.0200.CFUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 111642
LENGTH: 19
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Publication No. US20050246794A1

GENERAL INPORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Anaetasia
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/420,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.;
APPLICANT: Reynolds, Angela;
APPLICANT: Reynolds, Angela;
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 ACTCTGGAGTCCTCTGAGA 43
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Best Local Similarity 84.2
Matches 16, Conservative
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US-11-101-244-197226
                                                                                                                                                                                                                                                                                                                                ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1111642
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18.4%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 1.3e+02; ive 0; Mismatches 3; Indels
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US-11-101-244-716725/C

Sequence 716725, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Brocova, Anastasia

APPLICANT: Rynorova, Anastasia

APPLICANT: Rynorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

ITILE OF INVENTION: Functional and Hyperfunctional siRNA

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

TITLE OF INVENTION: 2005-04-07

FILE REFERENCE: 2005-04-07

PRIOR FILING DATE: 2005-04-07

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 716725

LENGTH: 1972
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 749629, Application US/11101244; Publication No. US20050246794A1; GENERAL INFORMATION: APPLICANT: Dharmacon, Inc.
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 619922
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                    25 ACTCTGGAGTCCTCTGAGA 43
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Matches 16; Conservative
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US-11-101-244-618922
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US-11-101-244-716725
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US-11-101-244-749629/c
                                                                                                                                                                                                                                 TYPE: RNA
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; Sequence 539604, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Khvorova, Anstasia
APPLICANT: Reynold, Angela
APPLICANT: Responder, Devin
APPLICANT: Beake, Devin
APPLICANT: Brainge, Stephen
TITLE OF INVERTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 05/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2002-01-0
PRIOR PILING DATE: 2002-11-14
; WUMBER: OF SEQ ID NOS: 1591911
; SEQ ID NO 539604

LENGTH: 19
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; Publication No. US20050246794A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scatinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 527824
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US-11-101-244-539604
                                                                                                                                                                                                                                                           ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-527824
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Matches 15; Conserv
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Matches 16; Conserv
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US-11-101-244-618922
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Best Local Similarity 84.2
Matches 16, Conservative
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CORGANISM: Homo sapiens
US-11-101-244-840452
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US-11-101-244-931449
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US-11-101-244-1006983/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Characton, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 06/502,050
PRIOR PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
IMMUTH: 19
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; Sequence 840452, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khyorova, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Argela
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
; TITLE PREFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-101-244-819751
; Sequence 819751, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; CURRENT FILING DATE: 2005-04-07; PRIOR APPLICATION NUMBER: 60/502,050; PRIOR PILING DATE: 2003-09-10; PRIOR APPLICATION NUMBER: 60/426,137; PRIOR FILING DATE: 2002-11-14; NUMBER OF SEQ ID NOS: 1591911; SEQ ID NO 749629; LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                  34 TCCTCTGAGAGGTAAAGAG 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                             19 TCTTCTTAGAGGTACAGAG 1
                                                                                                                                                                                                                                                                                                     Query Match 18.4
Best Local Similarity 84.2
Matches 16; Conservative
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                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-749629
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US-11-101-244-819751
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Best Local Similarity
Matches 13; Conserva
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Query Match
Best Local Similarity 63.2
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-11-101-244-1238798
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Best Local Similarity
Matches 16; Conserval
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US-11-101-244-1286557/c
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Sequence 1178034, Application US/11101244

Publication No. US20850246794A1

GENERAL INFORMATION:

APPLICANT: Khvorova, Anastaaia

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

APPLICANT: Scarings, Stephen

TITLE OF INVERTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2002-010

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SEQTWARE: Proprietary

SEQ ID NO 1178034
                                                                                                                                                                                                                                                      18.4%; Score 14.2; DB 1; Length 19; 84.2%; Pred. No. 1.3e+02; tive 0; Mismatches 3; Indels
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| Publication No. US20050246794a1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Responds, Purcional and Hyperfunctional siRNA |
| TITLE OF INVENTION: Punctional and Hyperfunctional siRNA |
| TITLE OF INVENTION: Punctional and Hyperfunctional siRNA |
| FILE REFERENCE: 13499US |
| CURRENT APPLICATION NUMBER: US/11/101,244 |
| CURRENT PAPLICATION NUMBER: 60/502,050 |
| PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1006983
LENGTH: 19
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                       16; Conservative
                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-101-244-1006983
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US-11-101-244-1178034
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Best Local Similarity
Matches 16; Conserva
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US-11-101-244-1238798
                                                                                                                                                                     TYPE: RNA
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iSequence 1257649, Application US/11101244

j Publication No. USCO050246794A1

j GENERAL INFORMATION:
   APPLICANT: Norova, Anastasia
   APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Leake, Devin
   APPLICANT: Scaringe, Stephen
   TILE OF INVENTION: Functional and Hyperfunctional siRNA
   TILE OF INVENTION: Functional and Hyperfunctional siRNA
   FILE REFRERENCE: 134990E
   CURRENT PILING DATE: 2005-04-07
   PRIOR APPLICATION NUMBER: 60/502,050
   PRIOR PILING DATE: 2005-09-10
   PRIOR PILING DATE: 2005-11-14
   NUMBER: OF SEQ ID NOS: 1591911
   SOFTWARE: Proprietary
   SEQ ID NO 1257649
   LENGITH: 19
   LENGITH: 19
   LENGITH: 19
   LENGITH: 19
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
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Pred. No. 1.3e+02;
4; Mismatches 3;
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APPLICANT: Dharmacon, Inc.
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1238798
LENGTH: 19
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Gaps

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Score 14.2; DB 1; Length 19;
Pred. No. 1.3e+02;
0; Mismatches 3; Indels
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Sequence 1508424, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Barmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Leake, Devin

TITLE OF INVENTION: Functional and Hyperfunctional sirNa

PILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT PILING DATE: 2005-04-07

PRIOR PILING DATE: 2005-09-10

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTHARE: Proprietary

LENGTHARE: Proprietary
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APPLICANT: Dharmacon, Inc.
APPLICANT: Chrorrova, Anastasia
APPLICANT: RAVOTOVA, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Respondis, Angela
APPLICANT: Respondis, Stephen
APPLICANT: Marshall, William
APPLICANT: Scarings, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT PILING DATE: 2005-03-18
PRIOR PLILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
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Publication No. US20050245475A1
                                                                                                                                                                                                                                                                                                                     23 CAACTCTGGAGTCCTCTGA 41
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     NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1402806
LENGTH: 19
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                ; ORGANISM: Homo sapiens
US-11-101-244-1402806
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US-11-101-244-1508424
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US-11-101-244-1508424/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1327450, Application US/11101244
; Publication No. US20050246794A1
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Exprolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devil iman
; APPLICANT: Marshall, William
; APPLICANT: Beake, Devil
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
; TITLE OF INVENTION: Punctional and Hyperfunctional
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1591911
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APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Acaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1286557
LENGTH: 19
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Matches 16; Conservative
                                                                                                                                TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-1286557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-101-244-1327450
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US-11-101-244-1402806/c
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0; Mismatches
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                         PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION WUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 518286
LENGTH: 19
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-083-784-518286
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US-11-083-784-527824
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US-11-083-784-539604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Khvorova, Anastasia
APPLICANT: Rhvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respective of the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 518286, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Charactasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional
CURRENT FILIA 3499US
CURRENT FILIA DATE: 2005-03-18
; FRIOR APPLICATION NUMBER: US/11/083, 784
; FRIOR FILING DATE: 2005-11-14
                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 68.4%;
Matches 13; Conservative
PRIOR FILING DATE: 2002-11-14
                             NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 197226
LENGTH: 19
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Best Local Similarity 84.24
Then 16; Conservative
                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-083-784-197226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-404601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-083-784-404601/c
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US-11-083-784-518286/c
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Score 14.2; DB 1; Length 19;
Pred. No. 1.3e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Education in the process of Applicant: Rhydrodg, Angela Applicant: Reynolds, Angela Applicant: Reynolds, Angela Applicant: Respective in the process of Applicant: Beake, Devin Applicant: Scarings, Stephen TILLE OF INVENTION: Functional and Hyperfunctional siRNA FILE REFERENT APPLICATION NUMBER: US/11/083,784 CURRENT FILING DATE: 2005-03-18 CURRENT FILING DATE: 2005-03-18 PRIOR APPLICATION NUMBER: US/10/714,333 PRIOR PLING DATE: 2003-11-14 PRIOR PLING DATE: 2003-11-14 PRIOR PLING DATE: 2003-11-14 NUMBER OF SEQ ID NOS: 1591911 SOFTWARE: Proprietary SEQ ID NO 527824
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Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: DAMACON, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Responds, Angela

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional sirNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784
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18.4%; Score 14.2; DB 1; Length 19;
ilarity 84.2%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 3; Indels
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Kryonold, Angela

APPLICANT: Eake, Devin

APPLICANT: Areadal, William

APPLICANT: Marchall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

TITLE OF INVENTION: Functional and Hyperfunctional

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: GO/502,050

PRIOR PLING DATE: 2003-11-14

PRIOR PLING DATE: 2003-01-10

PRIOR FILING DATE: 2003-01-10

PRIOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 749629

LENGTH: 19
                              TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                              FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 716725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 749629, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
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; Sequence 819751, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
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Best Local Similarity 84.2%;
Matches 16; Conservative
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APPLICANT: Khvorova, Anasi
APPLICANT: Reynolds, Ange.
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CORGANISM: Homo sapiens
US-11-083-784-716725
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US-11-083-784-749629
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Best Local Similarity
Matches 16; Conserv
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i Sequence 618922, Application US/11083784

i Publication No. US20550245475A1

i GENERAL INFORMATION:

APPLICANT: Beynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Beynolds, Angela

APPLICANT: Best, Devin

APPLICANT: Best, Devin

APPLICANT: Best, Devin

TITLE NO INVENTION: Functional and Hyperfunctional siRNA

TITLE REPERENCE: 13499US

CURRENT APPLICATION NUMBER: US/10/714,333

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PLING DATE: 2003-10-14

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

NUMBER OF ESQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 618922

LENGTH: 19922
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Pred. No. 1.3e+02;
1; Mismatches 3; Indels
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Pred. No. 1.3e+02;
5; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PLING DATE: 2003-11-14
PRIOR PLING DATE: 2003-11-14
PRIOR PLING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
SOFTWARE: PEDDITECTION NUMBER: 6/426,137
SOFTWARE: PEDDITECTION NUMBER: 6/426,137
LENGTH-10
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 GAGGTAAAGAGCCAGCGAA 60
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1 AAUCUUGAGUCUUCUGAGA 19
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Best Local Similarity 78.9%;
Matches 15; Conservative
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Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-539604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-083-784-618922
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Dharmacon, Inc.
Khvorova, Anastasia
Reynolds, Angela
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US-11-083-784-931449
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US-11-083-784-1006983
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Pred. No. 1.3e+02;
3; Mismatches 3; Indels
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Sequence 840452, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Revorova, Ansatasia

APPLICANT: Revorova, Ansatasia

APPLICANT: Revorova, Mariana

APPLICANT: Revorova, Mariana

APPLICANT: Responde, Angela

APPLICANT: Responde, Angela

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT APPLICATION NUMBER: US/10/714,333

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PLING DATE: 2003-11-14

PRIOR PLING DATE: 2003-11-14

PRIOR FILING DATE: 2003-10-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2002-11-14
               APPLICANT: Breake, Devilliam
APPLICANT: Breakell, William
APPLICANT: Scaringe, Stephen
ITLE OF INTENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR PLILIAGION NUMBER: US/10/714,333
PRIOR PLILIAGION NUMBER: 60/502,050
PRIOR PLILING DATE: 2003-03-10
PRIOR PLILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 19751
LENGTH: 19
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1 GGAGAGUCUGAGAGGUAA 19
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Best Local Similarity 68.4%;
Matches 13; Conservative
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SOFTWARE: Proprietary
SEQ ID NO 840452
LENGTH: 19
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-11-083-784-819751
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US-11-083-784-840452
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US-11-083-784-1178034/c

RESULT 105

; Sequence 931449, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:

US-11-083-784-931449

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23 CAACTCTGGAGTCCTCTGA 41
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Best Local Similarity 84.2%;
Matches 16; Conservative (
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US-11-083-784-1257649
                                                         S-11-083-784-1257649/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-083-784-1286557/c
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; Sequence 1238798, Application US/11083784
; GENERAL INFORMATION:
; APPLICATION NO. USCOOSO245475A1
; GENERAL INFORMATION:
; APPLICANT: EANCOONA, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sirNA
; TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
; PRICE REFRERENCE: 1349908
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT PILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR PILING DATE: 2003-11-14
; NUMBER: OF SCO ID NOS: 1591911
; SCOTTWARE: Proprietary
; LENGTH: 138798
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Pred. No. 1.3e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 18.4%; Score 14.2; DB 1; Length 19; 1 Similarity 84.2%; Pred. No. 1.3e+02; 16; Conservative 0; Mismatches 3; Indels
                                                                 GENERAL INFORMALION:
GENERAL INFORMALION:
GENERAL INFORMALION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reake, Devin
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
PRIOR PELING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PELING DATE: 2003-09-10
PRIOR PELING DATE: 2003-09-10
PRIOR PELING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1178034
LENGTH: 19
Sequence 1178034, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
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Best Local Similarity 63.2%;
Matches 12; Conservative
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US-11-083-784-1178034
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US-11-083-784-1238798
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Matches 16; Conserva
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US-11-083-784-1238798
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1286557, Application US/11083784
; Sequence 1286557, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
    APPLICANT: Diarmacon, Inc.
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Marshall, William
    FILIR REFERENCE: 13499US
    CURRENT APPLICATION NUMBER: US/11/083,784
    CURRENT FILING DATE: 2003-03-18
    FRIOR FILING DATE: 2003-11-14
    FRIOR PILING DATE: 2003-09-10
    FRIOR APPLICATION NUMBER: 60/426,137
    FRIOR APPLICATION NUMBER: 60/426,137
    FRIOR APPLICATION NUMBER: 2003-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SEQ ID NO 1286557
    LENGTH: 19
                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: GO/502,050
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1257649
LENGTH: 19
Sequence 1257649, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
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US-11-083-784-1508424, Application US/11083784

Sequence 1508424, Application US/11083784

Publication No. US/20050245475A1

GENERAL INFORMATION:
APPLICAMT: Brancon, Inc.
APPLICAMT: Reynolds, Angela
APPLICAMT: Leake, Devin
APPLICAMT: Bearlinge, Stephen
ITILE APPLICAMT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT PILIAG DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR PILING DATE: 2003-19-14

PRIOR PILING DATE: 2003-10-14

PRIOR PILING DATE: 2003-10-14

PRIOR FILING DATE: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 198424

LENGTH: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.4%; Score 14.2; DB 1; Length 19; Best Local Similarity 84.2%; Pred. No. 1.3e+02; Matches 16; Conservative 0; Mismatches 3; Indels
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Pred. No. 1.3e+02;
0; Mismatches 3;
0; Mismatches
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                                                   CTGA 41
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                                                                                              19 CAAATCTGAATTCCTCTGA 1
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Best Local Similarity 84.2
Matches 16; Conservative
  Matches 16; Conservative
                                                   23 CAACTCTGGAGTCC
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US-11-083-784-1508424
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US-10-310-914A-128507
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US-11-083-784-1402806/C

i Sequence 1402806, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
    APPLICANT: BANGON, Inc.
    APPLICANT: Reyrolds, Ansstasia
    APPLICANT: Reyrolds, Ansstasia
    APPLICANT: Reyrolds, Ansstasia
    APPLICANT: Reyrolds, Anstasia
    APPLICANT: Reyrolds, Anstasia
    APPLICANT: Marshall, William
    APPLICANTON Functional and Hyperfunctional siRNA
    TITLE OF INVENTION: Punctional and Hyperfunctional
    FILE OF INVENTION: Punctional and Hyperfunctional
    FILE OF INVENTION NUMBER: US/11/083,784
    CURRENT APPLICATION NUMBER: US/10/714,333
    PRIOR APPLICATION NUMBER: GO/502,050
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-10-14
    PRIOR PILING DATE: 2003-11-14
    NUMBER: OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    LENGRIH: 19
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                             APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
FRIOR RILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1327450
                                                                                                                                          Sequence 1327450, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: National Applicant: Rivorova, Anastasia
Applicant: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 CAGCGAAGCTGATGTCCTG 72
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19 GTGAAGATGAAGTCCTGTC 1
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84.2%;
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; ORGANISM: Homo sapiens
US-11-083-784-1402806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                    RESULT 109
US-11-083-784-1327450/c
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Best Local Similarity
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US-10-310-914A-128507/c

US-10-310-914A-128507/c

Sequence 128507, Application US/10310914A

Sequence 128507, Application US/10310914A

Publication No. US20060003322A1

Sequence 128507, Application No. US2006000332A1

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Biller, Kvuzat

APPLICANT: Biller, Willer, US0801

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 66087.0200. CPUS01

CURRENT APPLICATION WUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 128507

LENGTH: 20 ö ö Gaps Gaps

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US-101-914A-1313685/C
US-101-914A-1313685, Application US/10310914A
Sequence 1313685, Application US/10310914A
Sequence 1313685, Application US/10310914A
Sequence 1313685, Application US/2006000332A1
GENERAL INFORMATION: USO0600032A1
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: USOS thereof
TITLE OF INVENTION: USOS 138402
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1313685
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1087873, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
1 APPLICANT: Benefunded, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof

CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE PATENTIN version 3.3

LENGTH: 20
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Pred. No. 1.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                       0; Mismatches
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84.2%;
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 16; Conserv
; SEQ ID NO 971008
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-971008
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US-10-310-914A-1087873
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                                           US-10-310-914A-658051/c

| Sequence 658051, Application US/10310914A
| Publication Vo. US20060003322A1
| Publication No. US2006000332A1
| GRUERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| APPLICANT: Biller, Kvuzat
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| CURRENT APPLICATION NUMBER: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bhiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN version 3.3
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06007.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-112-06
NUMBER OF SEQ ID MOS: 1388402
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Score 14.2; DB 1;
84.2%; Pred. No. 1.3e+02;
tive 0; Mismatches 3;
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Pred. No. 1.3e+02;
0; Mismatches 3;
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; Sequence 833580, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-310-914A-971008/c
; Sequence 971008, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGGATACAACTCTGGAG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 CTGAGAGGTAAAGAGCCAG 56
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84.2%;
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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Best Local Similarity
Matches 16; Conserva
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US-10-310-914A-833580
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 658051
LENGTH: 20
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Sequence 43662, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION.
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION UNDER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dharmacon, Inc.
APPLICANT: Chrorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leaks. Gevin
APPLICANT: Leaks. Devin
APPLICANT: Acreball, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTOR: Punctional and Hyperfunctional siRNA
FILE REFRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 06/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.2%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 686616, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
                       PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION WUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 686616
LERNGTH: 19
PRIOR APPLICATION NUMBER: 60/502,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3
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Matches 14; Conservative
                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Homo gapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-083-784-686616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Proprietary
SEQ ID NO 686616
LENGTH: 19
                                                                                                                                                                                                                                                                                                                        US-11-101-244-686616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-083-784-686616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                               Sequence 1088471, Application US/10310914A
| Publication No. US20060003322A1
| GENERAL INPORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bhiler, Kvuzat
| TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
| TITLE OF INVENTION: USES TO SOURCE OF USES TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILLING DATE: 2002-112-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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US-11-101-244-686616
; Sequence 686616, Application US/11101244
; Publication No. US20550246/94A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khyorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reske, Devin
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.2%; Score 14; DB 1; Length 19; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1123448, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:
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Best Local Similarity 71.4%;
Matches 10; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1088471
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                                 US-10-310-914A-1088471
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LENGTH: 19
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Sequence 202536, Application US/10310914A

Sequence 202536, Application US/10310914A

Sequence 202536, Application No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Uses thereof
FILE REPERENCE: 06097.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 202536
LENGTH: 19
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| Sequence 760173, Application US/10310914A
| Sequence 760173, Application US/10310914A
| Publication No. US20060003322A1
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Kvuzat
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: Uses thereof
| FILE REFERENCE: 06687.0200.CPUS01
| CURRENT APPLICATION NUMBER: US/10/310,914A
| UNMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 760173
                                   Sequence 946707, Application US/10310914A

Publication No. US2006000332A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
Uses thereof
TITLE OF INVENTION:
Uses thereof
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 946707
LENGTH: 18
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Pred. No. 1.6e+02;
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Pred. No. 1.5e+02;
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88.2%;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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US-10-310-914A-946707
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US-10-914A-732261
US-10-914A-732261
Sequence 732261, Application US/10310914A
Federal Sequence 732261, Application US/10310914A
Federal INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
FILE APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
CURRENT PAPLICATION WOBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 73261
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; Sequence 815753, Application US/10310914A
; Sequence 815753, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Baller, Kvuzat
; TITLE OF INVENTION: Uses thereof
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PATEITING VERSION 3.3
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                               Score 14; DB 1; Length 20;
Pred. No. 1.3e+02;
4; Mismatches 0; Indels
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                                                                                                                                               Query Match 18.2%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                       64 GATGTCCTGTCAAG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 17.9
Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 13; Conserv
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; ORGANISM: Human
US-10-310-914A-815753
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US-10-310-914A-732261
                                                  ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-43662
SEQ ID NO 43662
LENGTH: 20
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Pred. No. 1.5e+02;
4; Mismatches 2; Indels
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Pred. No. 1.5e+02;
4; Mismatches 2; Indels
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APPLICANT: Charmeton, Inc.
APPLICANT: Charmeton, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Leake, Devin
APPLICANT: Cark, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 67079
LEMORTH: 19
                                                                                                                                                       APPLICANT: KNOWCOW, Anastasia
APPLICANT: KNOWCOW, Anastasia
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PRILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 14272
LENGTH: 19
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Publication No. US20050246794A1
GENERAL INFORMATION:
                           Sequence 14272, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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Best Local Similarity 64.7%;
Matches 11; Conservative
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Best Local Similarity 64.7%;
Matches 11; Conservative
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                                                                                                                               APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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| Publication No. US20060003322A1
| Publication No. US2006000332A1
| GENERAL INPORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| APPLICANT: Brider, Kvuzat
| TITLE OF INVENTION: Uses thereof
| TITLE NEFERENCE: 06087.0200.CPUS01
| TITLE NEFERENCE: 06087.0200.CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 785946, Application US/10310914A
Publication No. US20060003322A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
CURRENT APPLICATION UNDERF: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 785948
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                                                                                                                                                                 17.9%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 1.5e+02; Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                17 AAATAAGATGGCCTGGG 1
                                                                                                                                                                 Query Match 17.9
Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 11; Conserva
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US-10-310-914A-785948
                                                                    , ORGANISM: Human
US-10-310-914A-760173
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ORGANISM: Human
LENGTH: 19
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Score 13.8; DB 1; Length 19;
Pred. No. 1.5e+02;
4; Mismatches 2; Indels
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; Bequence 161088, Application US/11101244
; Publication No. US202050246794A1
; GENERAL INPORMATION:
   APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
   APPLICANT: Reynolds, Angela
   APPLICANT: Marball, William
   APPLICANT: Scaringe, Stephen
   TITLE OF INVENTION: Functional and Hyperfunctional sirny
   PILS REPERROR: 13499US
   CURRENT FILING DATE: 2005-00-07
   PRIOR PLICATION NUMBER: 60/426,137
   PRIOR PLICATION NUMBER: 2002-11-14
   SOFTWARE: Proprietary
   SOFTWARE: Proprietary
   LENGTH: 19
                                                                                                           APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-00-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARR: Proprietary
SEQ ID NO 160989
LENGTH: 19
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Best Local Similarity 64.7%;
Matches 11; Conservative
       Publication No. US20050246794A1
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US-11-101-244-160989
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US-11-101-244-161088
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-101-244-160889

Sequence 160889, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Ravorova, Ansatasia

APPLICANT: Ravorofa, Ansatasia

APPLICANT: Revnolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Leake, Devin

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REPREMENT: 344996, Stephen

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE SEPREMENT: 2005-04-07

FRICH APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PLING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SROID NO 160889
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                                                                                                       APPLICANT: Characon, Inc.
APPLICANT: Characon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolda, Angela
APPLICANT: Leake, Devin
APPLICANT: Marehall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FRICH REFREENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
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Sequence 98224, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 GAAGCTGATGTCCTGTC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAAGGGGAUGUCCUGU 17
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88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 GAAGGTGATGTCCTGGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.2 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-11-101-244-160889
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US-11-101-244-160989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-101-244-98224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.9%; Score 13.8; DB 1; Length 19; 70.6%; Pred. No. 1.5e+02;
APPLICANT: Education in the state of APPLICANT: Revnolds, Angela APPLICANT: Revnolds, Angela APPLICANT: Revnolds, Angela APPLICANT: Revnolds, Angela APPLICANT: Marchall, William APPLICANT: Marchall, William APPLICANT: Scaringe, Stephen TITLE OF INVENTION: Functional and Hyperfunctional siRNA; FILE REPERENCE: 13499US CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 219953
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Education Angela
APPLICANT: Edake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/420,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SGOTWARE: Proprietary
SEQ ID NO 276299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 276299, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
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Sequence 290226, Application US/11101244
; Publication No. US20550246794A1
; GENERAL INFORMATION:
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-101-244-219953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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US-11-101-244-276299
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; Sequence 197189, Application US/11101244
; Publication Wo. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Characon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Responds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional giRNA
; TITLE OF INVENTION: Functional and Hyperfunctional
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION FUNCES: 13499US
; CURRENT APPLICATION NUMBER: 05/502,050
; PRIOR FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2002-11-14
; NUMBER: OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 197189
; LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.9%; Score 13.8; DB 1; Length 19; 64.7%; Pred. No. 1.5e+02; tive 4; Mismatches 2; Indels
     APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolda, Angela
APPLICANT: Leake, Devin
APPLICANT: Responda, Angela
APPLICANT: Responda, Angela
APPLICANT: Responda, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 05/502,050
FRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 161190
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; Sequence 219953, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
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Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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US-11-101-244-161190
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US-11-101-244-197189
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--ANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

ITLE OF INVENTION: Mactional and Hyperfunctional girna

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 44405

ITYPE: PARENT PARENT PRIOR P
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17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Responded, Angela
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR FILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
IERNGTH: 19
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; Sequence 440203, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Knvorova, Anastasia
APPLICANT: Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 TCTGAGAGGTAAAGAGC 53
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
US-11-101-244-404405
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US-11-101-244-440203
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US-11-101-244-290240

Sequence 290240, Application US/11101244

Publication No. US20550246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Scarings, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REPREMENTE: 1349908R: 2005-04-07

PRIOR APPLICATION NUMBER: 60/622,050

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-10-11

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 290240

LENGTH: SEQ.
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                                                                                                                                                                                              APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERROR: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
SPRIOR PILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 290226
LENGTH: DATE
THENGTH: DATE
THENGTH:
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US-11-101-244-404405/c
; Sequence 404405, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anagtasia
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Best Local Similarity 82.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-101-244-290226
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; ORGANISM: Homo sapiens
US-11-101-244-290240
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 64.7%; Pred. No. 1.5e+02; Matches 11; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 727031, Application US/11101244
; Sequence 727031, Application US/11101244
; Publication No. U3202050246794A1
; GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Marball, William
    APPLICANT: Acatinge, Stephen
    TITLE OF INVENTION: Functional and Hyperfunctional siRNA
    TILE OF INVENTION: Punctional and Hyperfunctional siRNA
    FILE REFERENCE: 13499US
    CURRENT APPLICATION NUMBER: US/11/101,244
    CURRENT FILING DATE: 2005-04-07
    PRIOR PLIING DATE: 2003-09-10
    PRIOR PLIING DATE: 2003-09-10
    PRIOR PLIING DATE: 2003-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    SEQ ID NO 727031
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
TITLE OF INVENTION: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 681344
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Sequence 731099, Application US/11101244

PUBLICATION NO. USCOSO246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin
APPLICANT: Marshall, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAGCUGAGGUCCUGUGA 17
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                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-681344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-101-244-727031
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US-11-101-244-727031
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     APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT PERIORICATION NUMBER: 05/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SSETWARE: Proprietary
SEQ ID NO 524859
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Aszinge, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-14
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US-11-101-244-673690/c
| Sequence 673690, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Dhamacon, negation
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khovorova, Anastasia
APPLICANT: Krovorova, Anastasia
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TACAACTCTGGAGTCCT 37
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SOFTWARE: Proprietary
SEQ ID NO 673690
LENGTH: 19
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-11-101-244-524859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-101-244-673690
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US-11-101-244-681344
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Length 19;

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Score 13.8; DB 1; Length 19;
Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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Sequence 813171, Application US/11101244

SENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Dharmacon, Inc.
APPLICANT: Eake, Devin
APPLICANT: Reymolds, Angela
APPLICANT: Resmall, William
APPLICANT: Marball, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2003-00-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 813171
LENGTH: 19
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                    17.9%; Score 13.8; DB 1;
88.2%; Pred. No. 1.5e+02;
tive 0; Mismatches 2;
                FILE REFERENCE: 134990S
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 751095
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Publication No. US20050246794A1
GRNERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 CCTCTGAGAGGTAAAGA 51
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88.2%;
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Best Local Similarity 88.29
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-101-244-751095
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US-11-101-244-813171
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US-11-101-244-813171/c
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US-11-101-244-862664/c
                                                                                                                                                                                                                                                                            TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 731168, Application US/11101244

Sequence 731168, Application US/11101244

GENERAL INPORMATION:
APPLICANT: Charmeron, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Acaringe, Stephen
APPLICANT: Acaringe, Stephen
APPLICANT: Applicant Nunctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOPTWARE: Proprietary
SEQ ID NO 731168
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                   FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILLING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 19
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Sequence 751095, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION,

APPLICANT: Dharmacon, Inc.

APPLICANT: Rhyorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen
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Best Local Similarity 88.2.
Conservative
15; Conservative
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; ORGANISM: Homo sapiens
US-11-101-244-731168
                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-101-244-731099
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                                                                                                                                                                                                                                                                                                 TYPE: RNA ORGANISM:
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REPERRENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 941347
LENGTH: 19
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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US-11-101-244-941347
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US-11-101-244-959690
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US-11-101-244-966428
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; Sequence 900906, Application US/11101244
; Publication Wo. US2050246794A1
; GENERAL INFORMATION:
; APPLICANT: Rivorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TITLE OF INVERTION: Publicant and Hyperfunctional siRNA
; TITLE OF INVERTION NUMBER: US/11/101,244
; CURRENT PILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER: OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 900906
; LENGTH: 19
                                                                                                                                                                                                                                                                               17.9%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                     2; Indels
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Publication No. US20050246794A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Khvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                     0; Mismatches
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-862664
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Matches 15; Conserv
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US-11-101-244-941347/c
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PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 19
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                         ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1069062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-11-101-244-1149570
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US-11-101-244-1271626
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; Publication No. US20850246794A1
; GENERAL INFORMATION: US20850246794A1
; GENERAL INFORMATION: TOORWATION:
; APPLICANT: Ravorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Besnolds, Angela
; APPLICANT: Besnolds, Stephen
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TITLE OF INVERTION: Publicant and Hyperfunctional siRNA
; TITLE OF INVERTION NUMBER: US/11/101,244
; CURRENT APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER: OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1036369
                                                                                                                                                                                                                                                                                                      17.9%; Score 13.8; DB 1; Length 19; 82.4%; Pred. No. 1.5e+02; tive 1; Mismatches 2; Indels
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Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Marchall, William

APPLICANT: Marchall, William

APPLICANT: Marchall, William

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE REFERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFUMARE: Proprietary
SEQ ID NO 966428
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                 1 CAAACAAGACGGCCTGG 17
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                                                                                                                                                                                                                                                                                                    Query Match 17.9
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-966428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-101-244-1036369
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Matches 15; Conserv
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17.9%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 1.5e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 1149570, Application US/11101244
; Fublication No. US20050246794A1
; Fublication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.;
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Marball, William
; PIIL REFERENCE: 134990
; CURRENT FILING DATE: 2003-09-10
; PRIOR PLICATION NUMBER: 60/426,137
; PRIOR PLICATION NUMBER: 60/426,137
; RIOR PLING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SSOTIMARE: POPPLICATY
; SEQ ID NO 1149570
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64.7%; Pred. No. 1.5e+02;
ive 4; Mismatches 2; Indels
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT PELLOATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
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PRIOR APPLICATION NUMBER: 60/426,137
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Best Local Similarity 88.2%;
Matches 15; Conservative
                                PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1286517
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 AGCGAAGCTGATGTCCT
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                                                                                                                                                                                        TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1286517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-11-101-244-1299503
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; Sequence 1286508, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Darmacon, Inc.
; APPLICANT: Knvorova, Anstasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Responds, Angela
; APPLICANT: Bashall, William
; APPLICANT: Bashall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: 60/502,050
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR APPLICATION NUMBER: 60/426,137
; RIOR APPLICATION NUMBER: 60/426,137
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels
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Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT APPLICATION NUMBER: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION WUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1271626
LENGTH: 19
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Best Local Similarity 88.27
Best Local Similarity 88.27
Conservative
                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-101-244-1271626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-11-101-244-1286508
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US-11-101-244-1286517/c
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US-11-101-244-1299503/C
Sequence 1299503, Application US/11101244
Sequence 1299503, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Eake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2002-010
PRIOR PILING DATE: 2002-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE PEOPLICATY
INDRESSE OF SEQ ID NOS: 1591911
SOFTWARE PEOPLICATY
TUNDE PILING DATE: 2002-11-14
MUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: PEOPLICATY
TUNDE PILING DATE: 2002-11-14
SOFTWARE: PEOPLICATY
THOSE PEOPLICATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
   Length 19;
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US-11-101-244-1321159

i Sequence 1321159, Application US/11101244

j Publication No. US20050246794A1

i GENERAL INFORMATION:

i APPLICANT: Dharmacon, Inc.

j APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR PAPLICATION NUMBER: 60/502,050

PRIOR PILICATION NUMBER: 60/426,137
                                                            Indels
Score 13.8; DB 1;
Pred. No. 1.5e+02;
                                                            0; Mismatches
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Gaps

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Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 82.4%; Pred. No. 1.5e+02; Matches 14; Conservative 1; Mismatches 2; Indels
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; Sublication No. US20050346794A1
; Publication No. US20050346794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.;
; APPLICANT: Chorcova, Anaetasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Respective Stephen
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; RENOR PELICATION NUMBER: 60/426,137
; RENOR PELICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: PROPRIETATY
; LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 82.4%; Pred. No. 1.5e+02; Matches 14; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                      44 GGTAAAGAGCCAGCGAA 60
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     NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1359524
LERIGTH: 19
                                                                                                                                         ; ORGANISM: Homo sapiens
US-11-101-244-1359524
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US-11-101-244-1359621
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US-11-101-244-1359621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1334132, Application US/11101244
; Sequence 1334132, Application US/11101244
; GENERAL INFORMATION
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Ansstasia
; APPLICANT: Reynolds, Ansstasia
; APPLICANT: Reworlds, Ansstasia
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
; TITLE OF INVENTION: Punctional and Hyperfunctional
; PRIOR REPREMENT: 2005-04-07
; FILE OF INVENTION NUMBER: 60/402,050
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR PLING DATE: 2003-09-10
; PRIOR PLING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.9%; Score 13.8; DB 1; Length 19; 70.6%; Pred. No. 1.5e+02; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                   Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 70.6%; Pred. No. 1.5e+02; Matches 12; Conservative 3; Mismatches 2; Indels
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| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Characon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Responder, Devin
| APPLICANT: Responder, Stepholds
| APPLICANT: Scaringe, Stepholds
| APPLICANT: Marchall, William
| APPLICANT: Scaringe, Stephols
| APPLICANT: Marchall, William
| APPLICANT: Marchall, William
| APPLICANT: Marchall, William
| APPLICANT: Marchall, William
| APPLICANTON: Functional and Hyperfunctional siRNA FILE REPRENCE: 13499US
| CURRENT FILING DATE: 2005-04-07
| PRIOR APPLICATION NUMBER: 60/502,050
| PRIOR APPLICATION NUMBER: 60/426,137
| PRIOR PILING DATE: 2003-09-11-14
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1321159
LENGTH: 19
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Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                      TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1321159
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US-11-101-244-1334132
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Sequence 1453192, Application US/11101244
; Sequence 1453192, Application No. US20205246794A1
; Publication No. US202050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.;
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Resholds, Angela
; APPLICANT: Gake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
; FILE REPRENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 06/502,050
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR PILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 1591911

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                                                                                                                                                                                                                         Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 88.2%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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APPLICANT: Kivova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNa
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 05/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
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; Sequence 67079, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
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                                                                                                                                                                                                                                                                                                                                                                                  47 AAAGAGCCAGCGAAGCT
                                   LENGTH: 19
TYPE: RNA
CNGANISM: Homo sapiens
US-11-101-244-1565567
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SEQ ID NO 1565567
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; Sequence 1510975, Application US/11101244
; Publication No. US20550246794A1
; GENERAL INFORMATION:
; APPLICANT: Rivorova, Anastasia
; APPLICANT: Revorova, Anastasia
; APPLICANT: Revorova, Anastasia
; APPLICANT: Revorova, Anastasia
; APPLICANT: Revorova, Marshall, William
; APPLICANT: Beake, Devin
; TILLE OF INVENTION: Punctional and Hyperfunctional siRNA
; TILLE OF INVENTION: Punctional and Hyperfunctional
; TILLE OF INVENTION: Punctional and Hyperfunctional
; FILLE REFERENCE: 13499US
; CURRENT PILLING DATE: 2005-04-07
; PRIOR PILLING DATE: 2003-09-10
; PRIOR PILLING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOPTWARE: Proprietary
; LENGTH: 19
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US-11-101-244-1565567/C

Sequence 1565567, Application US/11101244

PUDLICATION NO. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dibramacon, Inc.

APPLICANT: Khyorova, Ansatasia

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFREENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT PILICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PILICATION NUMBER: 5002-11-14

NUMBER OF SEQ ID NOS: 1591911
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                                                                                                              TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1453192
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CRGANISM: Homo sapiens
US-11-101-244-1510975
SOFTWARE: Proprietary
SEQ ID NO 1453192
LENGTH: 19
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Best Local Similarity
Matches 14; Conserv
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US-11-101-244-1510975
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i Sequence 160889, Application US/11083784

j Publication No. US200245475A1

j GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Arrive Corrive Statings

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR FILING DATE: 2003-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98234.7 Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Seephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQTWARE: Proprietary
SEQ ID NO 99224
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2 CUGGAGUCUUCUGACAG 18
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 57079
LENGTH: 19
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                                                                                                                  TYPE: RNA
CRGANISM: Homo sapiens
US-11-083-784-67079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-98224
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Best Local Similarity
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US-11-093-784-160989
US-11-093-784-160989
US-11-093-784-160989
US-11-093-784-10083-18
US-11-04-04-10-19
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i Sequence 161088, Application US/11083784

j Publication No. US20050245475A1

i GENERAL INFORMATION.

j APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Punctional and Hyperfunctional sirNa

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784
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Pred. No. 1.5e+02;
4; Mismatches 2;
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 CGAAGCTGATGTCCTGT 73
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Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
CRGANISM: Homo sapiens
US-11-083-784-160889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-11-083-784-160989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorva, Anaetasia
APPLICANT: Kaynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respective to the control of the control 
       TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                          FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
FRIOR PILING DATE: 2003-09-10
FRIOR PILING DATE: 2003-10-10
FRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 219953, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 GCCAGCGAAGCTGATGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GCCAGAGUAGCUGAUGU 18
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; ORGANISM: Homo sapiens
US-11-083-784-197189
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US-11-083-784-219953
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US-11-083-784-276299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 161199, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Datarmacon, Inc.
; APPLICANT: Revnoids, Ansstasia
; APPLICANT: Revnoids, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION: Punctional and Hyperfunctional
; TITLE OF INVENTION: Punctional and Hyperfunctional
; PRIOR REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR PLILOR DATE: 2005-03-18
; PRIOR PLILOR DATE: 2003-01-11
; PRIOR PLILOR DATE: 2003-01-10
; PRIOR PLILOR DATE: 2003-01-11
; RIOR APPLICATION NUMBER: 60/426,137
; RIOR PLILOR DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARR: Proprietary
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPILERTY
LENGTHARE: PROPILERTY
LENGTHARE: 19
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Publication No. US20050245475A1
GENERAL INPORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
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Best Local Similarity 64.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-161190
                                                                                                                                                                                                                                                                                                                                                                                                                                                CRGANISM: Homo sapiens US-11-083-784-161088
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US-11-083-784-197189
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Dharmacon, Inc.
Khvorova, Anastasia
Reynolds, Angela
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US-11-083-784-290226

US-11-083-784-290226

Publication No. US205024475A1

GENERAL INFORMATION:

APPLICANT: KNYONOVA, Anastasia
APPLICANT: KNYONOVA, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Beak, Devinliam
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional sirNa
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT PLING DATE: 2003-01-0

PRIOR PILING DATE: 2003-01-0

PRIOR PLICATION NUMBER: 60/426,137

PRIOR PLICATION NUMBER: 60/426,137

PRIOR PLICATION NUMBER: 60/426,137

PRIOR PLICATION NUMBER: 60/426,137

SOFTWARE: Proprietary
SEQ ID NO 290226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.9%; Score 13.8; DB 1; Length 19; 82.4%; Pred. No. 1.5e+02; tive 1; Mismatches 2; Indel8
APPLICANT: Leake, Devin
APPLICANT: Maraball, William
APPLICANT: Scaringe, Stephen
TILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFRENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 2003-10-14
PRIOR PLING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 276299
LENGTH: 19
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US-11-083-784-290240
; Sequence 290240, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-083-784-276299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-290226
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA ORGANISM:
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Pred. No. 1.5e+02;
1; Migmatches 2; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INVENTATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Revnoids, Anastasia
APPLICANT: Revnoids, Angela
APPLICANT: Revnoids, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
TITLE OF INVENTION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 0S/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
SROFWARE: PROPRIETATY
SOFTWARE: Proprietary
SEQ ID NO 404405
LENGTH: 19
APPLICANT: Leafes, Devin
APPLICANT: Leafes, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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Best Local Similarity 82.4%;
Matches 14; Conservative
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US-11-083-784-290240
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ORGANISM: Homo sapiens
US-11-083-784-404405
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 88.2%; Pred. No. 1.5e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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Publication No. US20850245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/11/14,333
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: S001-114
SUFFRARE: Proprietary
SOFFWARE: Proprietary
LENGTH: 19
                                                                                                                                                                     APPLICANT: Dharmacon, Inc.
APPLICANT: Dharmacon, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolda, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marehall, William
APPLICANT: Marehall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT PILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
                                                                                    Sequence 673690, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-083-784-681344
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SEQ ID NO 673690
LENGTH: 19
                                                                 JS-11-083-784-673690/c
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                                                                       GENERAL INFURCATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: KNOTOVA, Anaetasia
APPLICANT: KNOTOVA, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Restringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
FRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PLING DATE: 2003-11-14
PRIOR PLILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
SPRIOR FILING DATE: 2003-11-14
SPRIOR FILING DATE: 2003-11-14
SPRIOR FILING DATE: 2002-11-14
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APPLICANT: Dharmacon, Inc.
APPLICANT: Revroids, Anastasia
APPLICANT: Revroids, Angela
APPLICANT: Revroids, Angela
APPLICANT: Respondis, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PELING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 524859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 524859, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION:
Sequence 440203, Application US/11083784
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                            Publication No. US20050245475A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-11-083-784-440203
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; ORGANISM: Homo sapiens
US-11-083-784-524859
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Matches 10; Conserv
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15; Conservative
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US-11-083-784-751095
                                                                                                                                                          RESULT 190
US-11-083-784-731168/c
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Matches
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US-11-083-784-731099/c

Sequence 731099, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Exprolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Leake, Devin

APPLICANT: Arguing Marshil, William

APPLICANT: Arguing Number (Stephen)

TITLE OF INVENTION: Punctional and Hyperfunctional sirNA

FILE REFERENCE: 134998

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PLING DATE: 2003-09-10

SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH. 10
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APPLICANT: Khorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Responds, Angela
APPLICANT: Maraball, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERROR: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: G0/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PLLING DATE: 2003-11-14
PRIOR PLLING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
                                                                                                                               Sequence 727031, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
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88.2%;
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Best Local Similarity 64.7
Matches 11; Conservative
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ORGANISM: Homo sapiens
US-11-083-784-727031
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CORGANISM: Homo sapiens
US-11-083-784-731099
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Best Local Similarity
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195-11-083-784-751095/C

1 Sequence 751095, Application US/11083784

2 Publication No. US20050245475A1

3 GENERAL INPORMATION:

4 APPLICANT: Dharmacon, Inc.

5 APPLICANT: Reynolds, Angela

5 APPLICANT: Reynolds, Angela

5 APPLICANT: Marchall, William

APPLICANT: Marchall, William

5 APPLICANT: Scaringe, Stephen

7 TITE OF INNENTION: Functional and Hyperfunctional 81RNA

7 FILE REFERENCE: 1349US

7 CURRENT APPLICATION NUMBER: US/11/083,784

7 CURRENT PILING DATE: 2003-01-18

7 PRIOR PILING DATE: 2003-01-14

7 PRIOR PILING DATE: 2003-09-10

7 PRIOR FILING DATE: 2003-11-14

7 PRIOR FILING DATE: 2003-11-14

7 NUMBER OF SEG ID NOS: 1591911

7 SEG ID NO 751095

7 LENGTH: 19
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; Sequence 731168, Application US/11083784
; Publication No. US2050245475A1
; GENERAL INPORMATION:
; APPLICANT: Diarmacon, Inc.;
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Respective to the propriate of the properties of the propriation of the propriation of the properties of the propriation of the properties of the p
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Pred. No. 1.5e+02;
0; Mismatches 2;
Mismatches
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                                                                                  24 AACTCTGGAGTCCTCTG 40
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                                                                                                                                                            18 AACTCTGAATTCCTCTG 2
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Best Local Similarity 88.2%;
Matches 15; Conservative
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US-11-083-784-731168
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; ORGANISM: Homo sapiens
US-11-083-784-862664
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; ORGANISM: Homo sapiens
US-11-083-784-900906
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US-11-083-784-900906
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                                                                                                                                                                                                                                                          Sequence 813171, Application US/11083784
; Sequence 813171, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
    APPLICANT: Rivorova, Anastasia
    APPLICANT: Rivorova, Anastasia
    APPLICANT: Revnolds, Angela
    APPLICANT: Revnolds, Angela
    APPLICANT: Revnolds, Angela
    APPLICANT: Beake, Devin
    APPLICANT: Scaringe, Stephen
    TITLE OF INVENTION: Functional and Hyperfunctional siRNA
    TITLE OF INVENTION: Punctional and Hyperfunctional
    FILE REFREENCE: 13499US
    CURRENT APPLICATION NUMBER: US/11/083,784
    CURRENT FILING DATE: 2005-03-18
    PRIOR APPLICATION NUMBER: 60/502,050
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2003-11-14
    PRIOR PILING DATE: 2002-11-14
    NUMBER: OF SQU ID NOS: 1591911
    SOFTWARE: Proprietary
    SEQ ID NO 813311
    LENGTH: 19
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US-11-083-784-862664/C

Sequence 862664, Application US/11083784

Publication No. US20650245475A1

GENERAL INFORMATION:

APPLICANT: Daramacon, Inc.

APPLICANT: Leake, Devin

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Scaringe, Scephen

ITILE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/10/714,333

FRIOR PLIING DATE: 2005-03-18

PRIOR PLIING DATE: 2003-11-14

PRIOR PLILING DATE: 2003-11-14

PRIOR PLILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 862664

LENGTH: 19
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17.9%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 1.5e+02; tive 0; Mismatches 2; Indels
                                                                                                              35 CCTCTGAGAGGTAAAGA 51
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                                                                                                                                            18 CTTCTGAGAGGTAAACA 2
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  Query Match
Best Local Similarity 88.23
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-813171
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US-11-083-784-813171/c
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| 17.14 | 17.14 | 17.14 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.24 | 18.2
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TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-966428
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US-11-083-784-1036369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 959690, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Scephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
   APPLICANT: Dharmacon, Inc.
   APPLICANT: Rhyorova, Anastasia
   APPLICANT: Reynolds, Angela
   APPLICANT: Marshall, William
   APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Scaringe, Stephen
   TILLS OF INVENTION: Punctional and Hyperfunctional siRNA
   FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION.

PILE REPRESENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                  27 TCTGGAGTCCTCTGAGA 43
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                                                                                                                                                                                                                                                                                                                     19 TCTTGAGTCCACTGAGA 3
                                                                        TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-941347
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US-11-083-784-959690
SOFTWARE: Proprietary
SEQ ID NO 941347
LENGTH: 19
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Pred. No. 1.5e+02;
1; Mismatches 2; Indele
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Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE OF INVENTION: Punctional and Hyperfunctional siRNA
CURRENT PLILING DATE: 2005-03-18

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/11/083,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dharmacon, Inc.
APPLICANT: Khorova, Anaetasia
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin Halliam
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-011-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1036369, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2002-11-14 NUMBER OF SEQ ID NOS: 1591911 SOFTWARE: Proprietary SEQ ID NO 966428 LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                    CAAACAAGAAGACCUGG 17
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Matches 15; Conservative
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US-11-083-784-1286508/C
US-11-083-784-1286508/C
i Sequence 1286508, Application US/11083784
i Publication No. US20050245475A1
i GENERAL INFORMATION:
APPLICANT: Diarmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Heake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
ITILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1286508
LENGTH: 19
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88.2%; Pred. No. 1.5e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 64.7%; Pred. No. 1.5e+02; Matches 11; Conservative 4; Mismatches 2; Indels
                                              PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1271626
     CURRENT APPLICATION NUMBER: US/11/083,784
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Revnova, Anastasia
APPLICANT: Revnova, Angela
APPLICANT: Revnouds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
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Best Local Similarity 88.2
Matches 15; Conservative
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US-11-083-784-1271626
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US-11-083-784-1286508
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US-11-083-784-1286517/c
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; Sequence 1149570, Application US/11083784
; GENERAL INFORMATION
; APPLICANT: DAIRMACON, Inc.
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION: Punctional and Hyperfunctional
; PRICA REPREMENT 2003-18
; CURRENT APPLICATION NUMBER: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-10-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2002-11-14
; SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 149570
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Publication No. US20050245475A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Chvorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Marshall, William

TITLE OF INVENTION: Punctional and Hyperfunctional siRNA; FILE REFERENCE: 13499US
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SEQ ID NO 1069062
; LENGTH: 19
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AGAUGAUGUCCUGGCAA 18
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US-11-083-784-1069062
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US-11-083-784-1149570
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Matches 11; Conserv
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US-11-083-784-1149570
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US-11-083-784-1271626
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Score 13.8; DB 1; Length 19;
Pred. No. 1.5e+02;
3; Mismatches 2; Indels
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Sequence 1334132, Application US/11083784

Publication No. USCOSC245475A1

GENERAL INFORMATION:
APPLICANT: Charmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Rexings, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-14

PRIOR FILING DATE: 2003-10-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: PROPILEATION NUMBER: 60/426,137

RIGHT APPLICATION NUMBER: 60/426,137

RIGHT APPLICATION NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

SOFTWARE: PROPILEATION NUMBER: 60/426,137

FRIOR FILING DATE: 2002-11-14

SEQ ID NO 134132

LENGHH: 19
                                APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scarkell, William
APPLICANT: Scarkell, William
APPLICANT: Scarkell, William
APPLICANT: Scarkell, William
APPLICANT: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1321159
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Pred. No. 1.5e+02;
3; Mismatches 2;
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Best Local Similarity 70.6%;
Matches 12; Conservative
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Best Local Similarity 70.6%;
Matches 12; Conservative
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US-11-083-784-1321159
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CORGANISM: Homo sapiens
US-11-083-784-1334132
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Sequence 1299503, Application US/11083784

Publication No. USCO05024547541

GENERAL INFORMATION:
APPLICANT: Charmacon, Inc.
APPLICANT: Revolds, Angela
APPLICANT: Revolds, Angela
APPLICANT: Revolds, Angela
APPLICANT: Beaching, Milliam
APPLICANT: Beaching, Stephen
APPLICANT: Gearing, Stephen
APPLICANT: Bearing, Stephen
APPLICANT: Bearing, Stephen
APPLICANT: Boulds: Number: US/11/083,784
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1299503

LINGTHEN OF TELLING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.9%; Score 13.8; DB 1; Length 19; 88.2%; Pred. No. 1.5e+02; tive 0; Mismatches 2; Indels
## APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Punctional and Hyperfunctional siRNA |
| FILE REFERENCE: 13499US |
| CURRENT APPLICATION NUMBER: US/11/083,784 |
| CURRENT PILING DATE: 2005-03-18 |
| PRIOR PILING DATE: 2003-11-14 |
| PRIOR PILING DATE: 2003-11-14 |
| PRIOR PILING DATE: 2003-09-10 |
| PRIOR PILING DATE: 2003-09-10 |
| PRIOR PILING DATE: 2003-09-10 |
| PRIOR PILING DATE: 2003-11-14 |
| WUMBER OF SEQ ID NOS: 1591911 |
| SOFTWARE: Proprietary |
| LENGTH: 19
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Sequence 1321159, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GAAGCTGATGTCCTGTC 74
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88.2%;
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Matches 15; Conservative
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US-11-083-784-1286517
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US-11-083-784-1299503
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Best Local Similarity
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Pred. No. 1.5e+02;
1; Mismatches 2; Indels
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17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Respirate, Devin

APPLICANT: Respirate, Pevin

APPLICANT: Respirate, Stephen

APPLICANT: Marshall, William

TITLE OF INVENTION: Functional siRNA

FILE REFERENCE: 13499US

CURRENT PILLOR DATE: 2005-03-18

PRIOR PILLOR DATE: 2003-11-14

PRIOR PILLOR APPLICATION NUMBER: 60/502,050

PRIOR PLING DATE: 2003-10-10

PRIOR PLING DATE: 2003-10-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTHARE: Proprietary

LENGTH: 19
                                                                                                                   APPLICANT: DATAMACON, INC.
APPLICANT: Khyorova, Anaetasia
APPLICANT: Khyorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANTON FUNCTIONAL BOOK Stephen
TITLE OF INVENTION: FUNCTIONAL UNMERR: US/11/083,784
CURRENT APPLICATION NUMBER: US/110/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PLILNG DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 1453192
LENGTH: 19
                      Sequence 1453192, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS AGCGAAGCTGATGTCCT 71
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Best Local Similarity 82.4%;
Matches 14; Conservative
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US-11-083-784-1453192
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US-11-083-784-1510975
US-11-083-784-1453192/c
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Sequence 1359621, Application US/11083784
Spublication No. US20850245475A1
GENERAL INFORMATION:
APPLICANT: RAVOROVA, Anastasia
APPLICANT: RAVOROVA, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Rewolds, Angela
APPLICANT: Leake Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908.
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR PRILOR DATE: 2005-01-14
PRIOR PRILING DATE: 2005-11-14
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2002-11-14
SPIOR FILING DATE: 2002-11-14
SPIOR FILING DATE: 2002-11-14
SPIOR FILING DATE: 2002-11-14
SPIOR FILING DATE: 2002-11-14
SOFTWARE: Proprietary
SEQ ID NO 1359621
SEQ ID NO 1359621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.9%; Score 13.8; DB 1; Length 19; Best Local Similarity 82.4%; Pred. No. 1.5e+02; Matches 14; Conservative 1; Mismatches 2; Indels
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                                                                APPLICANT: ALIVACOUS, ANGELA
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2003-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR PLILICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLILING DATE: 2003-11-14
PRIOR PLILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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                                                     Khvorova, Anastasia
Reynolds, Angela
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US-11-083-784-1359524
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ORGANISM: Homo sapiens
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61

45 GTAAAGAGCCAGCGAAG

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RESULT 209

1 GUGAAGAGCCAGUGAAG 17

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Sequence 1127226, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVERTION: Boinformatically detectable group of novel regulatory genes and
TITLE OF INVERTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
FILE REFERENCE: 2002-12-06
NUMBER OF SEQ ID NOS: 1188402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1127926
LENGTH: 18
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Publication No. US20060003322A1
Fublication No. US20060003322A1
FUBLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITUR OF INVENTION: Boloinformatically detectable group of novel regulatory genes and TITUR OF INVENTION: Uses thereof
TITUR OF INVENTION: Uses thereof
TITUR OF INVENTION: Uses 10310,914A
CURRENT PAPLICANTON NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 715225
LENGTH: 19
APPLICANT: Benewich, Isaac
APPLICANT: Benewich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 819956
LENGTH: 18
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Pred. No. 1.7e+02;
1; Mismatches 1; Indels
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Best Local Similarity 86.7%;
Matches 13; Conservative
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1 GAGUGCUCUGAGAGG 15
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; ORGANISM: Human
US-10-310-914A-715225
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                                                                                                                                                                                                                                             TYPE: RNA
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Pred. No. 1.5e+02;
0; Mismatches 2; Indels
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Pred. No. 1.7e+02;
1; Mismatches 1; Indels
                                                        Sequence 1565567, Application US/11083784

| CARLEAUL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Beake, Devin
| APPLICANT: Marshall, William
| TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
| FILE REFERENCE: 13499US
| CURRENT FILING DATE: 2005-03-18
| PRIOR APPLICATION NUMBER: 60/502,050
| PRIOR PILING DATE: 2003-09-10
| PRIOR PLING DATE: 2003-09-10
| PRIOR PLING DATE: 2003-09-10
| PRIOR PLING DATE: 2003-11-14
| NUMBER OF SEG ID NOS: 1591911
| SOFTWARE: Proprietary
| LENGTH: 1965557
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; Sequence 819956, Application US/10310914A
; Publication No. US20060003322A1
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88.2%;
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86.7%;
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Best Local Similarity 86.7
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Best Local Similarity 88.2
Matches 15; Conservative
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US-11-083-784-1565567
                        RESULT 211
US-11-083-784-1565567/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-310-914A-730939
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ORGANISM: Human
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UG-10-310-914A-1268592/c
UG-10-310-914A-1268592/c
Sequence 1268592, Application US/10310914A
Sequence 1268592, Application US/10310914A
Sequence 1268592, Application US/10310914A
Sequence 1268592, Application No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Benindermatically detectable group of novel regulatory genes and TITLE OF INVENTION: USES thereof
TITLE OF INVENTION: USES thereof
TITLE OF INVENTION: USES thereof
TITLE OF INVENTION: USES (0607.0200.CPUS01)
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1268592
LENGTH: 19
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Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof
                  APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION WUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1058236
LENGTH: 19
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80.0%; Pred. No. 1.6e+02;
iive 2; Mismatches 1;
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Pred. No. 1.6e+02;
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.4%
Best Local Similarity 80.0%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.7
Matches 13; Conservative
APPLICANT: Bentwich, Isaac
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                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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US-10-310-914A-1053707
US-10-310-914A-1053707
Sequence 1053707, Application US/10310914A
; Sequence 1053707, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1384402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1053707
                                                                                                                                                                                                                                                   RESULT 216
US-10-310-914A-751334
US-10-310-914A-751334
US-10-310-914A-751334
Sequence 751334, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: 0500.0200.0200.0201
CURRENT PELICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 751334
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 1; Length 19; Pred. No. 1.6e+02;
                        Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
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                                                                           1; Indels
                                                                           1; Mismatches
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US-10-914A-1058236
; Sequence 1058236, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                        17.4%;
86.7%;
                                                                                                                            2 AAACAAGACGGCCTG 16
                                                                                                                                                            22 ACAACTCTGGAGTCC 36
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                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 73.3
Matches 11; Conservative
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                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053707
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US-10-310-914A-751334
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Best Local S
Matches 13
                        Query Match
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                                                        US-11-101-244-24159/C

US-11-101-244-24159/C

Sequence 24159, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Ascaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional sirNA

FILE REFERENCE: 13499US

CURRENT APPLICATION WUMBER: 60/502,050

PRIOR FILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SEQ ID NO 24159

LEAGTH: 19
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respicion No. 131011101
APPLICANT: Respicion No. 131011
APPLICANT: Respicion No. 131011
APPLICANT: Beachall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Narshall, William
APPLICANT: Boaringe, Stephen
ITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
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Best Local Similarity 93.3
Matches 14; Conservative
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US-11-101-244-24159
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US-11-101-244-34612
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| Sequence 1370512/c
| Sequence 1370512, Application US/10310914A
| Publication No. US20060003322A1
| Publication No. US20060003322A1
| Publication No. US2006000332A1
| Publication No. US2006000332A1
| Publication No. US2006000332A1
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| APPLICANT: Britisty Normatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof
| TITLE OF INVENTION: uses thereof
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Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 1.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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| APPLICANT: Revoctor, Anastasia | APPLICANT: Revoctor, Anastasia | APPLICANT: Revoctor, Anastasia | APPLICANT: Revoctor, Angela | APPLICANT: Leake, Devin |
| APPLICANT: Leake, Devin | APPLICANT: Marchall, William | APPLICANT: Marchall, William | APPLICANT: Marchall, William | APPLICANT: Marchall, William | APPLICANT: Scaringe, Stephen | TITLE OF INVENTION: Functional and Hyperfunctional sirna | FILE REPERRICE: 13499US | CURRENT APPLICATION NUMBER: US/11/101,244 | CURRENT FILING DATE: 2003-09-10 | PRIOR APPLICATION NUMBER: 60/502,050 | PRIOR APPLICATION NUMBER: 60/426,137 | PRIOR PELING DATE: 2002-11-14 | NUMBER OF SEQ ID NOS: 1591911 | SOFTWARE: Proprietary | TONOR: 1591911 | TONOR: TONOR
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Sequence 24060, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
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ORGANISM: Human
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; ORGANISM: Homo saplens
US-11-101-244-219414
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ORGANISM: Homo sapiens
US-11-101-244-276236
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US-11-101-244-219414
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US-11-101-244-387184
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; Sequence 199690, Application US/11101244
; Publication No. US2050246794A1
; GRNERAL INFORMATION:
; APPLICANT: Chorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Beake, Devin
; APPLICANT: Beake, Devin
; APPLICANT: Beake, Devin
; APPLICANT: Marshall, William
; APPLICANT: ANDER: 14499US
; CURRENT PILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 199690
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
4; Mismatches 1; Indels
                                                                                  GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.
APPLICANT: Rhyorova, Anastasia
APPLICANT: Rhyorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Respectively.
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: 13499US
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 5002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 88668
                                             ; Sequence 88668, Application US/11101244
; Publication No. US20050246794A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 CGAAGCTGATGTCCT 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAACAAGACGACCU 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-199690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-88668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                         US-11-101-244-88668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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RESULT 227

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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 73.3%; Pred. No. 1.6e+02; Matches 11; Conservative 3; Mismatches 1; Indels
                                                                         APPLICANT: Characton, Inc.
APPLICANT: Rivorova, Anastasia
APPLICANT: Reynolda, Angela
APPLICANT: Resynolda, Angela
APPLICANT: Resynolda, Angela
APPLICANT: Resynolda, Angela
APPLICANT: Restant, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11.14
SOFTWARE: Proprietary
SEQ ID NO 219414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolda, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANTON: FUNCATION: FUNCTIONAL
CURRENT FILING FUNCATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 276236
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 276236, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
Sequence 219414, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAAACAAGACGGCCT 15
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Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 86.7%; Pred. No. 1.6e+02; Matches 13; Conservative 1; Mismatches 1; Indels
                                         APPLICANT: Chronocon, Inc.
APPLICANT: Rhyorova, Anaetesia
APPLICANT: Rhyorova, Anaetesia
APPLICANT: Reynolda, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
IENGTH: 19
    US20050246794A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 TAAAGAGCCAGCGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 TAAAGAGCCAGCGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-11-101-244-387392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
US-11-101-244-387492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-101-244-410730/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-101-244-387492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 387289, Application US/11101244
; Publication No. US2050246794A1
; Publication No. US2050246794A1
; Publication No. US2050246794A1
; Publication No. US2050246794A1
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVERTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: 60/502,050
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SQCTWARE: Proprietary
; SQCTWARE: Proprietary
; SQCTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                 APPLICANT: Dharmacon, Inc.
APPLICANT: Khorova, Anaetasia
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                             FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
SOFTWARE: Proprietary
SEQ ID NO 397184
Sequence 387184, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 231
US-11-101-244-387392
; Sequence 387392, Application US/11101244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.4%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 UAAAGAGCCUGCGAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UAAAGAGCCUGCGAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 TAAAGAGCCAGCGAA 60
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Best Local Similarity 86.7°
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-11-101-244-387184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 230
US-11-101-244-387289
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                                                                            APPLICANT: Characon, Inc.
APPLICANT: RAVOCOVA, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Ansthall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 387492
Sequence 387492, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 410730, Application US/11101244; Publication No. US20050246794A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02; Live 0; Mismatches 1; Indels
                                                                                          APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT PELLOR DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 411027
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 512370, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-101-244-527876/c
; Sequence 527876, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
                                Khvorova, Anastasia
Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 GAGTCCTCTGAGAGG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 ACAACTCTGGAGTCC 36
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-411027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 236
US-11-101-244-512370/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-101-244-512370
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US-11-10-244-410929/C

US-11-10-244-410929/C

Sequence 410929, Application US/11101244

Publication No. US20050246794A1

GENERAL INNORMATION:

APPLICANT: NewTolds, Angela

APPLICANT: RewTolds, Angela

APPLICANT: Leake, Devin

APPLICANT: RewTolds, Angela

APPLICANT: RewTolds, Angela

APPLICANT: RewTolds, Stephen

APPLICANT: RewTolds, Stephen

APPLICANT: Restring National and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT FILING DATE: 2005-04-07

PRIOR FILING DATE: 2003-09-10

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 410929

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                          APPLICANT: Khorova, Anastasia
APPLICANT: Khorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILER REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
SEQ ID NO 410730
LENGTH: 19
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US-11-101-244-411027/c
; Sequence 411027, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 GAGTCCTCTGAGAGG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 GAGTCCTCTGAGAGG 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 cacrecrercacars 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                           APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-11-101-244-410730
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US-11-101-244-410929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 14; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 14
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Gaps

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APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scarling Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-11
SOFTWARE: Proprietary
SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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         Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.35
...hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-11-101-244-550822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Homo sapiens
US-11-101-244-550923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 241
US-11-101-244-581627
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US-11-101-244-550923
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US-11-101-244-539325

Sequence 539325, Application US/11101244

Publication No. US20550246794A1

GENERAL INPORMATION:

APPLICANT: Rivorova, Anastasia

APPLICANT: Revnolda, Anastasia

APPLICANT: Scaringe, Stephen

ITILE OF INVENTION: Punctional and Hyperfunctional sirna

FILE REFREERENT 349918

CURRENT PILING DATE: 2005-04-07

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2003-10-11

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 539325

LENGTH: 19
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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Pred. No. 1.6e+02;
5; Mismatches 1; Indels
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
FILB REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 527876
LENGTH: 19
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; Publication No. US20050246794A1
; GENERAL INFORMATION:
GAPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 TGATGTCCTGTCAAG 77
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3 UCAUGUCCUGUCAAG 17
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-527876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-539325
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17.4%; Score 13.4; DB 1; Length 19; 73.3%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                       Sequence 550923, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Norova, Anastasia
APPLICANT: Revnoids, Anastasia
APPLICANT: Responds, Anastasia
APPLICANT: Leake, Devin
FITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 06/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 581627, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Kivorova, Anaerasia
; APPLICANT: Reynolds, Angela
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Gaps
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                                                                                                                                                                                                                                                                                                                                                    Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 60.0%; Pred. No. 1.6e+02; Matches 9; Conservative 5; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 710507, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
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Reynolds, Angela
Leake, Devin
Marshall, William
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                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AAGCTGATGTCCTGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.08
Matches 12; Conservative
                                                                                                                                                                                                                                                                             TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-680973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 244
US-11-101-244-686033
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Pred. No. 1.6e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.4%; Score 13.4; DB 1; Length 19; 66.7%; Pred. No. 1.6e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Enablescui, .....
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENT APPLICATION NUMBER: US/11/101,244
CURRENT APPLICATION NUMBER: 06/502,050
PRIOR PELLING DATE: 2005-010
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 62448
LENGTH: 19
                       APPLICANT: Markell, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
TITLE OF INVENTION: Punctional and Hyperfunctional sirNA
CURRENT FILING DATE: 149908
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 581627
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US-11-101-244-680973
Sequence 680973, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 624448, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                            17.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 TCTGAGAGGTAAAGA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.4
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.4
Best Local Similarity 73.3
Matches 11; Conservative
             Leake, Devin
                                                                                                                                                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-11-101-244-581627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-101-244-624448
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TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                     FILE REPERRICE: 1349905
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                           46 TAAAGAGCCAGCGAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 UNANGAGGCAGCGAN 15
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.7%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.7%
Matches 13, Conservative
                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-101-244-785114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-11-101-244-785140
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                                                                                                                                                                                                                                                           TYPE: RNA
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US-11-10-244-710553

US-11-10-244-710553

Sequence 710553, Application US/11101244

Publication No US20050246794A1

GENERAL INFORMATION:

APPLICANT: Beaken Devin Horizon, Inc.

APPLICANT: Revnolds, Angela

APPLICANT: Leake, Devin APPLICANT: Leake, Devin APPLICANT: Responds, Angela

APPLICANT: APPLICANT: Warshall, William APPLICANT: Responds, Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 1349908

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2005-04-07

PRIOR PILING DATE: 2003-09-10

PRIOR PILING DATE: 2002-11-14

SOPTWARE: Proprietary

SEQ ID NO 710553

LENGITH: 1953

LENGITH: 19
                                                                                                                                                                                                                                                                                                                                                          Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
## APPLICANT: Scaringe, Stephen
## TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
## FILER REFERENCE: 13499US
## CURRENT APPLICATION NUMBER: US/11/101,244
## CURRENT FILING DATE: 2005-04-07
## PRIOR PPLICATION NUMBER: 60/502,050
## PRIOR PPLICATION NUMBER: 60/426,137
## RIOR PLIING DATE: 2002-11-14
## NUMBER OF SEQ ID NOS: 1591911
## SOFTWARE: Proprietary
## SEQ ID NO 710507
## ILENGTH: 19
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US-11-101-244-785114
; Sequence 785114, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorcva, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
                                                                                                                                                                                                                                                                                                                                                            cch 17.4%;
al Similarity 93.3%;
14; Conservative (
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il Similarity 93.3%;
14; Conservative
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                                                                                                                                                                                                                                                                            TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-710507
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US-11-101-244-710553
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Best Local Similarity
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Best Local Similarity
Matches 14; Conserva
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17.4%; Score 13.4; DB 1; Length 19; 86.7%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indels
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                 Sequence 18140, Application US/11101244
; Sequence 18140, Application US/11101244
; Publication No. US202050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.;
; APPLICANT: Khorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Marball, William
APPLICANT: WINGHER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-09-10
; PRIOR PILING DATE: 2003-11-14
; SOFTWARE: PROPILETANT
; SOFTWARE: PROPILETANT
; SOFTWARE: PROPILETANT
; SEQ ID NO 785140
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; Sequence 795267, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Diarmacon, Inc.
; APPLICANT: Reyrolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Searinge, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sirNA
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s Sequence 972375, Application US/11101244

publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Bharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Beake, Devin
APPLICANT: Leake, Devin
APPLICANT: Archinal and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2005-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 972375
LENGTH: 19
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Pred. No. 1.6e+02;
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Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
FILE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
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CURRENT APPLICATION NUMBER: US/11/101,244
                                 PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SCOFTWARE: Proprietary
SEQ ID NO 878459
LENGTH: 19
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60.0%;
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Best Local Similarity 60.03
Matches 9; Conservative
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Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-101-244-878459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-972375
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US-11-101-244-972474/c
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; Fublication Wo. US2050246794A1
; GENERAL INFORMATION: US2050246794A1
; GENERAL INFORMATION: TOURS
; APPLICANT: CHORONA, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Responded
; APPLICANT: Responded
; APPLICANT: Leake, Devin
; APPLICANT: Barnall, William
; APPLICANT: Barnall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TITLE OF INVERTION: Punctional and Hyperfunctional siRNA
; TITLE OF INVERTION NUMBER: US/11/101,244
; CURRENT PILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; RIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER: OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 833429
                                                                                                                                                                                                                                                                                                                                             17.4%; Score 13.4; DB 1; Length 19; 60.0%; Pred. No. 1.6e+02; tive 5; Mismatches 1; Indels
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; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Charmacon, Inc.
; APPLICANT: Rhyorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
                CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR PILING DATE: 2003-09-10
FRIOR PILING DATE: 2003-09-10
FRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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| CAAAGCUGAUGUCCU 18
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Best Local Similarity 60.0
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-11-101-244-795267
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CORGANISM: Homo sapiens
US-11-101-244-833429
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US-11-101-244-878459
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US-11-101-244-833429
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PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOOTWARE Proprietary
SEQ ID NO 1034219
LENGTH: 19
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CORGANISM: Homo sapiens
US-11-101-244-1034219
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CORGANISM: Homo sapiens
US-11-101-244-1036393
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US-11-101-244-1012488
is Sequence 1012489, Application US/11101244
j Publication No. US20050246794A1
j GRNEALL INCORMATION:
j APPLICANT: Revnolds, Angela
j APPLICANT: Revnolds, Angela
j APPLICANT: Leake, Devin
j APPLICANT: Leake, Devin
j APPLICANT: Resnolds, Angela
j APPLICANT: Resnolds, Euchen
j APPLICANT: Leake, Devin
j APPLICANT: Resnolds, Resphen
j TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
j FILE REFRENCE: 13499US
j CURRENT APPLICATION NUMBER: 2005-04-07
j PRIOR APPLICATION NUMBER: 2005-04-07
j PRIOR FILING DATE: 2003-09-10
j PRIOR FILING DATE: 2002-11-14
j NUMBER: OF SEQ ID NOS: 1591911
scoptware: Proprietary
j SEQ ID NO 1012488
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PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 19
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GAAGAUGAUGUCCUG 16
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Best Local Similarity 93.3
Matches 14; Conservative
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US-11-101-244-972474
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US-11-101-244-1012488
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Best Local Similarity
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US-11-101-244-1034219/c
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US-11-101-244-1036393
i Sequence 1036393, Application US/11101244
i Publication No. US20050246794A1
i GRAREAL INFORMATION:
i APPLICANT: Darmacon, Inc.
i APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
ITILE OP INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 00/502,050
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR PILING DATE: 2005-04-07
FRIOR PILING DATE: 2005-11-14
NUMBER: OF SEQ ID NOS: 1591911
SEQ ID NO 1036393
LENGTH: 19
Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 1.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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| Sequence 1155168, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Chrozrowa, Ansatasia
| APPLICANT: Khrozrowa, Ansatasia
| APPLICANT: Reynolds, Angela
| APPLICANT: Marehall, William
| APPLICANT: Marehall, William
| APPLICANT: Geatinge, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional sirNA
| FILE REFERENCE: 13499US
| CURRENT APPLICATION NUMBER: US/11/101,244
| CURRENT PILING BATE: 2005-04-07
| PRIOR APPLICATION NUMBER: 60/502,050
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Publication No. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Drawcoon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Mastasia

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                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Pred. No. 1.6e+02;
0; Mismatches 1;
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1249609
LENGTH: 19
                                                                                                                                                                                                                                                                                                                 17.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GAAGCTGATGTCCTG 72
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Best Local Similarity 93.3
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                     TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1249609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-101-244-1326829
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US-11-101-244-1327400/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
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Sequence 1235172, Application US/11101244

PUBLICATION O. US20050246794A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Leake, Devin

APPLICANT: Barball, William

APPLICANT: Reynolds, Number

APPLICANT: Marshall, William

APPLICANT: Marchall, William

APPLICANT: Marchall, William

APPLICANT: Marchall, William

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 2002-11-14

NUMBER: OF SEQ ID NOS: 1591911

SEOFTWARE: Proprietary

SEQ ID NO 1233172
                                                                                                                                                                                                                                                                                                                                       Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 66.7%; Pred. No. 1.6e+02; Matches 10; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1249609, Application US/11101244
; Publication No. US20050246794A1
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Punctional and Hyperfunctional
; TITLE OF INVENTION: Punctional and Hyperfunctional
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT PAPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
   PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION WUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 155168
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAACUCUGGUGUCCU 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AACAAGACGGCCTGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CAACTCTGGAGTCCT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.37
...rhes 14; Conservative
                                                                                                                                                                                                                        TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1155168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-101-244-1235172
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US-11-101-244-1235172/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 259
US-11-101-244-1249609/c
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NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1351972
LENGTH: 19
                                                                                                                    ; ORGANISM: Homo sapiens
US-11-101-244-1351972
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US-11-101-244-1359582
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Khyorova, Anaetasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REPRENCE: 13499US
CURRENT FILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ. IN NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1351972, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Krynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
ITILE OF INVENTION: Punctional and Hyperfunctional
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT PILING DATE: 2005-04-07
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1327433, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                               Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1327400
                                                                                                                                                                                                                                                                                                           58 GAAGCTGATGTCCTG 72
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                                                                                                                                                                                                                                                                                                                                                       18 CAAGCTCAGGTCCTG 4
                                                                                                                TYPE: RNA
CRGANISM: Homo sapiens
US-11-101-244-1327400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-11-101-244-1327433
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| SECTION | 1900 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911 | 1911
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RESULT 269
US-11-10-244-1512594/C
isquence 1512594, Application US/11101244
isquence 1512594, Application US/11101244
isquence 1512594, Application US/11101244
isquence 1512594, Application US/11101244
isquence 1512594, Application, Inc.
isquence Dharmacon, Inc.
isquence Theorem Character, Devin
isquence Theorem Carlon Control of Applicant: Represe, Devin
isquence Theorem Carlon Control of Thrian Applicant: Scaringe, Stephen
itTILE OF INVENTION: Functional and Hyperfunctional siRNA
itTILE OF INVENTION NUMBER: US/11/101,244
isquence Application NUMBER: 60/502,050
ipplication Application NUMBER: 60/502,050
ipplication Application NUMBER: 60/426,137
ipplication Prints Date: 2003-09-10
ipplication Prints Date: 2003-09-10
ipplication NUMBER: Proprietary
issued ID NO: 1512594
                                                                                                                                                                                                 Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 1.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1492356, Application US/11101244

Fublication No. US20050246794A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respective, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Reynolds, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: 60/502,050
PRIOR PLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2003-09-10
PRIOR PLICATION NUMBER: 60/426,137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                           27 TCTGGAGTCCTCTGA 41
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                                                          ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1435574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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Best Local Similarity
Matches 14; Conserv
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SEQ ID NO 1435574
LENGTH: 19
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US-11-10-244-1418701
Sequence 1418701, Application US/11101244
Sequence 1418701, Application US/11101244
GENERAL INFORMATION:
APPLICANT: CANDERATION:
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Resental, William
APPLICANT: Resental, William
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Warshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVERTION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGIN: WARSHARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.4%; Score 13.4; DB 1; Length 19; 73.3%; Pred. No. 1.6e+02; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                             Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 86.7%; Pred. No. 1.6e+02; Matches 13; Conservative 1; Mismatches 1; Indels
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US-11-101-244-1435574/C

is Sequence 1435574, Application US/11101244

is Publication No. US20050246794A1

is GENERAL INFORMATION:

is APPLICANT: Diarmacon, Inc.

is APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

is APPLICANT: Marshall, William

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

ITILE OF INVERTION: Functional and Hyperfunctional siRNA

FILE REFREENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT PILICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PILICA DATE: 2003-09-10

PRIOR PILICATION NUMBER: 60/426,137

PRIOR PILICATION NUMBER: 60/426,137

PRIOR PILICATION NUMBER: 000-11-14

NUMBER OF SEQ ID NOS: 1591911
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                                                                                                                                                                                                                                                                                                                                                                                            46 TAAAGAGCCAGCGAA 60
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Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1418701
                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-101-244-1359676
SOFTWARE: Proprietary
SEQ ID NO 1359676
LENGTH: 19
                                                                                                             TYPE: RNA
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1560555
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; Publication No. US2050246794A1
; Publication No. US2050246794A1
; GENERAL INFORMATION:
; APPLICANT: Characon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Bearings, Stephen
; TITLE OF INVERTION: Functional and Hyperfunctional siRNA
; TILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT PILING DATE: 2005-04-07
; PRIOR PILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER: OF SEQ ID NOS: 1591911
; SEQ ID NO 1560555
; LENGTH: 19
                                                                                                     17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           Sequence 1522587, Application US/11101244

Sequence 1522587, Application US/11101244

Publication No. US20050246794A1

GENERAL INFORMATION

APPLICANT: Controva, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Beake, Devin

APPLICANT: Beake, Devin

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/101,244

CURRENT PILING DATE: 2005-04-07

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PILING DATE: 2002-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1522587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.4%; Score 13.4; DB 1; Length 19; 80.0%; Pred. No. 1.6e+02; tive 2; Mismatches 1; Indel8
                                                                                                                                                                                       18 GGATACAACTCTGGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 CTGAGAGGTAAAGAG 52
                                                                                                                                                                                                                16 GGATACAACTCTGAA 2
                                                                                                                      Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
                 TYPE: RNA
CORGANISM: Homo sapiens
US-11-101-244-1512594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1522587
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Matches 12; Conserva
                                                                                                                                                                                                                                                                                          RESULT 270
US-11-101-244-1522587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 271
US-11-101-244-1560555
LENGTH: 19
                                                                                                       Query Match
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Query Match

17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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| Sequence 1570074, Application US/11101244
| Sequence 1570074, Application US/11101244
| Publication No. US20050246794A1
| GENERAL INFORMATION:
| APPLICANT: Brancoon, Inc.
| APPLICANT: Reynolds, Angela
| APPLICANT: Marshall, William
| APPLICANT: Scaringe, Stephen
| ITER REPRENCE: 13499US
| CURRENT FILING DATE: 2005-04-07
| PRIOR PILING DATE: 2003-09-10
| PRIOR PILING DATE: 2003-11-14
| NUMBER OF SEQ ID NOS: 1591911
| SOFTWARE: Proprietary
| SEQ ID NO 1570074
| TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Reyrolds, Angela
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
APPLICANT: Beake, Devin
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2003-09-10
PRIOR PLICATION NUMBER: 60/502,050
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
PRIOR PLICATION NUMBER: 60/426,137
SEQ ID NO 1570662
LENGTH: 19
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Publication No. US20050246794A1
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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                                                                                                         1 CAAACAAGACGGCCT 15
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Gaps
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                                                                                                                                            Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 93.3%; Pred. No. 1.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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is Sequence 34612, Application US/11083784

is Publication No. US20050245475A1

is GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Revords, Anaetasia

APPLICANT: Revords, Anaetasia

APPLICANT: Marehall, William

APPLICANT: Marehall, William

APPLICANT: Marehall, William

APPLICANT: Scaring, Stephen

ITILE OF INVENTION: Punctional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT APPLICATION NUMBER: US/10/714,333

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911
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Publication No. US20050245475A1
GENERAL INFORMATION:
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                                  ; ORGANISM: Homo sapiens
US-11-083-784-24060
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US-11-083-784-24159
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US-11-083-784-24060/C

Sequence 24060, Application US/11083784

Publication No. US20550245475A1

GENERAL INFORMATION:
APPLICANT: Brancon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scarings, Scephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/10/714,333
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR PLING DATE: 2003-10-10
FRIOR PLING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
FRIOR PLING DATE: 2002-11-14
SOFTWARE: Proprietary
SOFTWARE: Proprietary
SOFTWARE: Proprietary
SOFTWARE: Proprietary
LENGTH: 19
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US-11-101-244-1590808
is sequence 1590808. Application US/11101244
j Publication No. US20050246794A1
j GENERAL INFORMATION:
i APPLICANT: Darmacon, Inc.
j APPLICANT: Reynolds, Angela
j APPLICANT: Reynolds, Angela
j APPLICANT: Leake, Devin
j APPLICANT: Scaringe, Stephen
j APPLICANT: Scaringe, Stephen
j TITLE OF INVERTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
j CURRENT APPLICATION NUMBER: US/11/101,244
j CURRENT PILING DATE: 2005-04-07
pRIOR FILING DATE: 2002-11-14
j NUMBER OF SEQ ID NOS: 1591911
j SOFTWARE: Proprietary
j SEQ ID NO 1590808
j LEMENT: 19
                                                                                                          Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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                                                                                                      Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
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US-11-101-244-1590808
; ORGANISM: Homo sapiens
US-11-101-244-1570074
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TYPE: RNA
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17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.6e+02;
4; Mismatches 1; Indels
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j Geguence 88666, Application US/11083784

j GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.
    APPLICANT: Reynolds, Angela
    APPLICANT: Marshall, William
    APPLICANT: Marshall, William
    APPLICANT: Marshall, William
    APPLICANT: WarrION: Punctional and Hyperfunctional siRNA
    TITLE OF INVENTION: Punctional and Hyperfunctional
    PILE REPERENCE: 13499US
    CURRENT APPLICATION NUMBER: US/11/0114,333
    PRIOR APPLICATION NUMBER: US/10/714,333
    PRIOR PILING DATE: 2003-11-14
    PRIOR PLING DATE: 2003-09-10
    PRIOR PLING DATE: 2003-09-10
    PRIOR PLING DATE: 2003-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SOFTWARE: Proprietary
    FENNING: PRIOR DATE: PROPRIETARY
    NUMBER OF SEQ ID NOS: 1591911
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.;
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respective Sequency
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILER REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/11/14,333
FRIOR PILING DATE: 2003-11-14
FRIOR PILING DATE: 2003-09-10
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                                                                        TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-34612
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SOFTWARE: Proprietary
SEQ ID NO 34612
LENGTH: 19
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Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.; APPLICANT: Revrolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-11
SOFTWARE: PLOSTIBLE SOUTH APPLICATION NUMBER: 60/426,137
PRIOR PLING DATE: 2003-09-11
SOFTWARE: PROPILE SOUTH APPLICATION NUMBER: 2003-09-11
SOFTWARE: PROPILE SOUTH APPLICATION NUMBER: 01-14
SOFTWARE: 01-14
SOFTWARE: PROPILE SOUTH APPLICATION NUMBER: 01-14
SOFTWARE: 01-14
SOFTWARE
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; Sequence 219414 Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 199690
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
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Best Local Similarity 86.79
Matches 13; Conservative
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US-11-083-784-199690
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US-11-083-784-219414
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Query Match
17.4%; Score 13.4; DB 1;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1;
                                 CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-10-14
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH, 19
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; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Chorcova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Marin Marshall, William
           CURRENT APPLICATION NUMBER: US/11/083,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 UAAAGAGCCUGCGAA 16
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Best Local Similarity 86.7*
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-083-784-387289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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; Sequence 387184, Application US/11083784

; Publication No. US20050245475A1

; GENERAL INFORMATION:
; APPLICANT: Barmacon, Inc.;
; APPLICANT: Revolds, Anstasia
; APPLICANT: Revolds, Anstasia
; APPLICANT: Revolds, Anstasia
; APPLICANT: Leake Devin
; APPLICANT: Leake Devin
; APPLICANT: Leake Devin
; TILLE OF INVENTION: Functional and Hyperfunctional siRNA
; TILLE OF INVENTION: Punctional and Hyperfunctional siRNA
; FILLE REFERENT 2003-18
; CURRENT APPLICATION NUMBER: US/10/714,333
; PRIOR PLILING DATE: 2005-03-18
; PRIOR PLILING DATE: 2003-19-10
; PRIOR FILING DATE: 2003-19-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387184
; LENGTH: DATE: DATE: TOPLICATION NUMBER: EVALORIS APPLICATION APP
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Pred. No. 1.6e+02;
3; Mismatches 1; Indels
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; Publication No. US20050245475A1
; GENERAL INPORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marball, William
; APPLICANT: Marball, William
; APPLICANT: Marball, William
; APPLICANT: Searinge, Stephen
; TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 276236
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.3%;
Matches 11; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                              TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-276236
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US-11-083-784-387184
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US-11-083-784-387289
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iSequence 387392, Application US/11083784
j Publication No. US20050245475A1
s GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respective, Devin
APPLICANT: Beake, Devin
APPLICANT: Scarings, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-10-14
PRIOR FILING DATE: 2003-10-14
PRIOR FILING DATE: 2002-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 387392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.4%; Score 13.4; DB 1; Length 19; 86.7%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indels
Length 19;
                                        Indels
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; Sequence 512370, Application US/11083784 ; Publication No. US20050245475A1
          Reynolds, Angela
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US-11-083-784-411027/c
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US-11-083-784-410730/C

Sequence 410730, Application US/11083784

Publication No. US20550245475A1

GENERAL INFORMATION:

APPLICANT: Diarmacon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Scaringe, Stephen

TITLE OF INVESTION: Functional and Hyperfunctional siRNA

PILE REFERENCE: 13499US

CURRENT PILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: US/10/714,333

PRIOR PLILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2002-11-14

NUMBER: WE PROPRIED TO NUMBER: 60/426,137

PRIOR FILING DATE: 2002-11-14

NUMBER: Proprietary

SEQ ID NO 410730

LENGTH: 19
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
## APPLICANT: Scaringe, Stephen
## TITLE OF INVENTION: Punctional and Hyperfunctional siRNA
## FILE REFREENCE: 13499US
## CURRENT APPLICATION NUMBER: US/11/083,784
## CURRENT FILING DATE: 2005-03-18
## PRIOR APPLICATION NUMBER: US/10/714,333
## PRIOR PELICATION NUMBER: 60/502,050
## PRIOR FILING DATE: 2003-09-10
## PRIOR FILING DATE: 2003-09-10
## NUMBER OF SEQ ID NOS: 1591911
## NUMBER OF SEQ ID NOS: 1591911
## SEQ ID NO 387492
## LENGTH: 19
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; Sequence 410929, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-410730
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US-11-083-784-387492
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APPLICANT: Republic R
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APPLICANT: KNOWOVA, Anaetesia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-10-10
FRIOR FILING DATE: 2003-11-14
SHOR FILING DATE: 2002-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LINNGTH: 19
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APPLICANT: Dharmacon, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 GAGTCCTCTGAGAGG 45
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-083-784-410929
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US-11-083-784-411027
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Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
5; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5:08022, Application US/11083784
; Publication No. US20050245475A1
; Publication No. US20050245475A1
; Publication No. US20050245475A1
; Publication No. US20050245475A1
; APPLICANT: Diarmacon, Inc.
; APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Acathage, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: 05/502,050
PRIOR PLING DATE: 2003-10-14
; PRIOR PLING DATE: 2003-10-14
; PRIOR PLING DATE: 2003-11-14
; PRIOR PLING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 550822
; LENGTH: 19
17.4%;
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Best Local Similarity 60.09
Matches 9, Conservative
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Best Local Similarity 73.3
Matches 11; Conservative
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US-11-083-784-550822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-083-784-539325
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17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 290
US-11-083-784-527876/C

Sequence 527876, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Bharmacon, Inc.
APPLICANT: Revorova, Anastasia
APPLICANT: Revorova, Anastasia
APPLICANT: Revorova, Mastasia
APPLICANT: Revorova, Mastasia
APPLICANT: Revorova, Mastasia
APPLICANT: Responde, Angela
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: MARSHER: US/11/083,784
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROPRIECATY
SEQ ID NOS: 1591911
                       APPLICANT: Khyorova, Ansatasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Searinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
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Best Local Similarity 93.3%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ACAACTCTGGAGTCC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AAGCTGATGTCCTGT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                              tryPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-512370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-083-784-527876
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LENGTH: 19
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RESULT 291

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US-11-03-04448

Sequence 624448, Application US/11083784

Sequence 624448, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Beancon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Leake, Devin

APPLICANT: Beanch, Devin

APPLICANT: BOINVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 13499US

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: 05/50,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PLING DATE: 2003-09-10

PRIOR PLING DATE: 2003-09-10

PRIOR PLING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.4%; Score 13.4; DB 1; Length 19; 66.7%; Pred. No. 1.6e+02; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence (19073), Application US/11083784

Publication No. US2005045475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Beynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Respect Searinge, Stephen
ITITLE OF INVENTION: Functional and Hyperfunctional siRNA
ITITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 134.99US
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/14,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-11
SOFTWARE: Proprietary
SEQ ID NO 680973
INVENT BENTALLY
INVENT BENTALLY
SEQ ID NO 680973
INVENT BENTALLY
INVENT BE
                                        1 UCUCAGAGGUAAAGA 15
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Best Local Similarity 66.77
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-083-784-624448
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US-11-083-784-680973
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Pred. No. 1.6e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 73.3%; Pred. No. 1.6e+02; Matches 11; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PLING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
IERNOTH: 19
                                                                                                                  Sequence 55023, Application US/11083784

Bublication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Rhyorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Respicit, Angela

APPLICANT: Beach, Devin

APPLICANT: Beach, Devin

APPLICANT: Beach, Devin

APPLICANT: Beach, Devin

APPLICANT: Marshall, William

FILE REFERENCE: 13499US

CURRENT APPLICATION NUMBER: US/10/714,333

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2003-10-11

PRIOR PILING DATE: 2003-10-11-14

PRIOR PILING DATE: 2003-10-11-14

NUMBER OF SEQ ID NOS: 1591911

SEQ ID NO 550923

LENGTH: 19
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; Sequence S81627, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 73.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 GGAGTCCTCTGAGAG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-550923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-581627
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17.4%; Score 13.4; DB 1; Length 19;

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17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                      Length 19;
                                                                                                                                                                                                                                                                                                                                       Sequence 7.025.3, Application US/11083784

Publication No. US202050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.;
APPLICANT: Reynolds, Angela
APPLICANT: Arguell, William
APPLICANT: Scaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499UG
CURRENT APPLICATION NUMBER: US/11/014,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PELING DATE: 2003-09-10
PRIOR PELING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 710553
LENGTH: 19
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APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Responds, Angela
APPLICANT: Beake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR PLILING DATE: 2003-01-14
PRIOR PLILING DATE: 2003-09-10
PRIOR PLILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 785114
                                                                                                            1; Indels
                                                Score 13.4; DB 1;
Pred. No. 1.6e+02;
0; Mismatches 1;
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                                                      Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                  61
                                                                                                                                                                                                                     3 AAAGAGCCAGAGAAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-083-784-785114
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US-11-083-784-710507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 298
US-11-083-784-710507
i Sequence 710507, Application US/11083784
j Publication No. US20550245475A1
j GENERAL INFORMATION:
APPLICANT: Diaramacon, Inc.
APPLICANT: Revnoids, Ansetasia
APPLICANT: Revnoids, Ansetasia
APPLICANT: Respondis, Angela
APPLICANT: Respondis, Angela
APPLICANT: Respondis, Angela
APPLICANT: Respondis, Angela
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
FILE OF INVENTION: Functional and Hyperfunctional
FILE OF INVENTION NUMBER: US/11/083,784
CURRENT APPLICATION NUMBER: US/10/714,333
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR FILING DATE: 2003-11-14
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR FILING DATE: 2003-10-14
SRIOR FILING DATE: 2003-11-14
NUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: PROPRIECATY
SEQ ID NO 710507
                                                                                                                                                                                                         US-11-083-784-686033

US-11-083-784-686033

Sequence 686033, Application US/11083784

Publication No. US20550245475A1

GENERAL INFORMATION:

APPLICANT: Dharmacon, Inc.

APPLICANT: Revorova, Ansetasia

APPLICANT: Revorova, Ansetasia

APPLICANT: Revorova, Ansetasia

APPLICANT: Revorova, Mastasia

APPLICANT: Revorova, Mastasia

APPLICANT: Revorova, Mastasia

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Renctional and Hyperfunctional siRNA

FILE OF INVENTION: Functional and Hyperfunctional

FILE OF INVENTION: Punctional and Hyperfunctional

FILE OF INVENTION NUMBER: US/11/083,784

CURRENT PILING DATE: 2005-03-18

FRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-10-14

PRIOR FILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SEQ ID NO SEQ ID NOS: 1591911

SEQ ID NO SEG033
                               1; Indels
Best Local Similarity 60.0%; Pred. No. 1.6e+02; Matches 9; Conservative 5; Mismatches 1
                                                                                                            3 AGGCUGAUGUCCUGU 17
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                                                                                  59 AAGCTGATGTCCTGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-083-784-686033
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Query Match
Best Local Similarity 66.7%;
Matches 10; Conservative
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 795267
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CAAAGCUGAUGUCCU 18
                                                                                                                                                                                                                                9; Conservative
                                                                                                               ; ORGANISM: Homo sapiens
US-11-083-784-795267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-833429
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-11-083-784-878459
                                                                                              TYPE: RNA
                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                          Sequence 785140, Application US/11083784
; Sequence 785140, Application US/11083784
; Publication No. US20050245475A1
; GREREAL INFORMATION:
; APPLICANT: Bytorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Best Devin
; APPLICANT: Boaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; FRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-10-10
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; RIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785-140
                                                                                                               17.4%; Score 13.4; DB 1; Length 19; 86.7%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dharmacon, Inc.
APPLICANT: Ribarmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Bearinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REPERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR PILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-083-784-795267
; Sequence 795267, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INPORMATION:
                                                                                                                                                                                                         46 TAAAGAGCCAGCGAA 60
                                                                                                                                                                                                                                                   1 UNANGAGGCAGCGAN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UAAAGAGGCAGCGAA 16
                                                                                                               Query Match 17.4
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                     TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-785114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-083-784-785140
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Best Local Similarity
LENGTH: 19
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US-11-083-784-1034219/c
; Sequence 1034219, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Anastasia
; APPLICANT: Reynolds, Angela
  PRIOR APPLICATION NUMBER: US/10/714,333
                    PRIOR FILING DATE: 2003-11-14
PRIOR PLING DATE: 2003-11-14
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2002-10
PRIOR PLING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE PROPRIETARY
SEQ ID NO 972474
LENGTH: 19
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Best Local Similarity 66.7%;
Matches 10; Conservative
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Matches 14; Conservative
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US-11-083-784-1012488
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US-11-083-784-1012488
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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US-11-083-784-972474/C
; Sequence 972474, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Reynolds, Angela
; APPLICANT: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Ceake, Devin
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION: WURSER: US/11/083,784
; CURRENT APPLICANT APPLICANT APPLICANT APPLICANT
; TITLE REFERENCE: 13499US
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APPLICANT: Khvorova, Angelsa
APPLICANT: Reyrolds, Angels
APPLICANT: Reyrolds, Angels
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT PILING DATE: 2005-03-18
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 972375, Application US/11083784; Publication No. US20050245475A1; GENERAL INFORMATION: APPLICANT: Dharmacon, Inc.
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION WUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SEQ ID NO 818459
LENGTH: 19
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93.3%;
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Best Local Similarity 60.0*
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Best Local Similarity 93.3,
Best Local 14; Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-972375
                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-11-083-784-878459
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US-11-083-784-972375/c
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Pred, No. 1.6e+02;
4; Mismatches 1; Indels
17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1012488, Application US/11083784

Sequence 1012488, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reyrolds, Angela
APPLICANT: Marchall, William
APPLICANT: Marchall, William
APPLICANT: Application Number: US/11/083,784

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PLING DATE: 2003-11-14

PRIOR PLING DATE: 2003-11-14

PRIOR PLING DATE: 2003-11-14

SPRIOR FILING DATE: 2002-11-14

SOFTWARE: PROPRICATION NUMBER: 60/426,137

PRIOR APPLICATION NUMBER: 60/426,137

PRIOR PLING DATE: 2002-11-14

SOFTWARE: PROPRICATOR

SOFTWARE: LENGTH: 19
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APPLICANT: Marshall, William
APPLICANT: Garringe, Stephan
ITTLE OF INVENTION: Functional and Hyperfunctional siRNA
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23 CAACTCTGGAGTCCT 37
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Matches 10; Conservative
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US-11-083-784-1155168
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US-11-083-784-1235172
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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Sequence 1036393, Application US/11083784

Publication No. USC050245475A1

GENERAL INFORMATION:
APPLICANT: Brown Ansetasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349998

TITLE OF INVENTION: Functional and Hyperfunctional
FILE OF INVENTION: Punctional and Hyperfunctional
FILE OF INVENTION NUMBER: US/11/083,784

CURRENT APPLICATION NUMBER: US/10/714,333

PRIOR PILING DATE: 2003-01-14

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NOS: 1591911

SCOUTHANTS: PROPRICATY
SEQ ID NO 1034942
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FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
FRIOR PILING DATE: 2003-11-14
FRIOR PILING DATE: 2003-05-10
FRIOR PILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1034219
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Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
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Matches 14; Conservative
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US-11-083-784-1034219
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; ORGANISM: Homo sapiens
US-11-083-784-1036393
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US-11-083-784-1155168
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APPLICANT:

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Score 13.4; DB 1; Length 19;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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APPLICANT: Charmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Khvorova, Anastasia
APPLICANT: Keryolds, Angela
APPLICANT: Keryolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Carringe, Stephen
ITILE OF INVENTION: Punctional and Hyperfunctional siRNA
FILE REFRERENCE: 134990US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
SRIOR FILING DATE: 2002-11-14
SOFTWARE: PROPRIECTION NUMBER: 60/426,137
FRIOR FILING DATE: 2002-11-14
SOFTWARE: PROPRIECTION NUMBER: 60/426,137
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR FILING DATE: 2002-11-14
FRIOR FILING DATE: 2002-11-14
FRIOR FILING DATE: 2003-100
FRIOR FILING D
Publication No. US20050245475A1
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Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 GAAGCTGATGTCCTG 72
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Best Local Similarity 93.3
Matches 14; Conservative
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US-11-083-784-1327400
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US-11-083-784-1327433
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; Sequence 1326829, Application US/11083784
; Publication No. US20850245475A1
; GENERAL INFORMATION:
; APPLICANT: Barmacon, Inc.;
APPLICANT: Rivorova, Anstasia
; APPLICANT: Rivorova, Anstasia
; APPLICANT: Revnolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; TITLE OF INVENTION: Functional and Hyperfunctional
; FILE REFREENCE: 13499US:
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR PILING DATE: 2003-11-14
; PRIOR PILING DATE: 2003-11-14
; RIOR PILING DATE: 2002-11-14
; RIOR PILING DATE: 2002-11-14
; RIOR APPLICATION NUMBER: 60/426,137
; RIOR PILING DATE: 2002-11-14
; SEQ ID NO 1326829
; LENGTH: 19
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                                                                                                             APPLICANT: Scatinge, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILLE REFERENCE: 13499US
FILLE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR FILLING DATE: 2003-11-14
FRIOR FILLING DATE: 2003-01-10
FRIOR FILLING DATE: 2003-09-10
FRIOR APPLICATION NUMBER: 60/426,137
FRIOR FILLING DATE: 2002-11-14
FRIOR FILLING DATE: 2002-11-14
SEACH FILLING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PROprietary
LENGTH: 19
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   Khvorova, Anastasia
                                                                Leake, Devin
Marshall, William
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                                   Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 GAAGCTGTTGTCCTG 1
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-083-784-1249609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo mapienm
US-11-083-784-1326829
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US-11-083-784-1326829/c
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US-11-083-784-1327400/c
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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i Sequence 1359582, Application US/11083784

j GENERAL INFORMATION:
    APPLICANT: Dharmacon, Inc.
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Responds, Angela
    APPLICANT: Reynolds, Angela
    APPLICANT: Responds, Stephen
    APPLICANT: Scaringe, Stephen
    APPLICANT: Arrive Scaringe, Stephen
    TITLE REFERENCE: 13499US
    CURRENT APPLICATION NUMBER: US/11/083,784
    CURRENT FILING DATE: 2005-03-18
    PRIOR FILING DATE: 2003-11-14
    PRIOR APPLICATION NUMBER: 60/520,050
    PRIOR FILING DATE: 2003-11-14
    NUMBER OF SEQ ID NOS: 1591911
    SOFTWARR: POPPLICATY
                                   Sequence 1351972. Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Chrorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Resholl, William
APPLICANT: General, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: US/10/714,333
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-11-14
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2003-09-10
FRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SOFTWARE: 19972
LENGTH: 19
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Best Local Similarity 93.3%;
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-11-083-784-1351972
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US-11-083-784-1359582
                           1-083-784-1351972/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1359582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.4%; Score 13.4; DB 1; Length 19; 86.7%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indels
                                                                GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Anastesia
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Responds, Angela
APPLICANT: Mareball, William
APPLICANT: Gcaringe, Stephen
ITILE OF INVENTION: Functional and Hyperfunctional siRNA
ITILE OF INVENTION: Functional and Hyperfunctional
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1359676
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1418701, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Reynolds, Angela
APPLICANT: Reynolds, Angela
APPLICANT: Respect Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT FILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR PLING DATE: 2003-11-14
PRIOR PLING DATE: 2003-10-10
PRIOR FILING DATE: 2003-11-14
SURING BATE: 2002-11-14
SURTHARE: PRODITEATY
SURTHARE: PRODITEATY
Sequence 1359676, Application US/11083784
Publication No. US20050245475A1
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Best Local Similarity 86.7%
Matches 13; Conservative
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Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-083-784-1359676
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                           Publication No. US20
GENERAL INFORMATION:
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US-11-083-784-1522587

US-11-083-784-1522587

Sequence 152287, Application US/11083784

Publication No. US20050245475A1

GENERAL INFORMATION:

APPLICANT: Brancon, Inc.

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Beake, Devin

APPLICANT: Scaringe, Stephen

TITLE OF INVENTION: Functional and Hyperfunctional siRNA

FILE REFREENCE: 1349908

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT FILING DATE: 2005-03-18

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR PILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

SEQ ID NO 152287

LENGRIH: PROPRICATY

SEQ ID NO 152287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR PLING DATE: 2003-09-10
PRIOR PLING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
LENGTH: 19
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                                                                                                                                   27 TCTGGAGTCCTCTGA 41
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Best Local Similarity 93.3
Matches 14; Conservative
                             Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-083-784-1512594
Query Match
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                                                                                                                                                                                                                                      Sequence 1435574/C

Sequence 1435574, Application US/11083784

Publication No. USCO050245475A1

GENERAL INFORMATION:
APPLICANT: Datamacon, Inc.
APPLICANT: Revolds, Ansstasia
APPLICANT: Revolds, Ansstasia
APPLICANT: Revolds, Ansstasia
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 1349908
FILE REFERENCE: 1349908
CURRENT APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2005-01-0
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2002-11-14
MUMBER: OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1435574

LENGTH: 19
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US-11-083-784-1492356/C
Sequence 1492356, Application US/11083784
APPLICANT: Edword, Inc.
APPLICANT: Reynold, Angela
APPLICANT: Reynold, Angela
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFREENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
FRIOR APPLICATION NUMBER: 60/502,050
FRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/426,137
FRIOR APPLICATION NUMBER: 60/426,137

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                                54 CAGCGAAGCTGATGT 68
                                                                     1 CAGUGAAGCUGAUGU 15
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US-11-083-784-1492356
                                                                                                                                                                                                        RESULT 320
US-11-083-784-1435574/C
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17.4%; Score 13.4; DB 1; Length 19; 93.3%; Pred. No. 1.6e+02; Live 0; Mismatches 1; Indel8
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                   RESULT 322
US-11-083-784-1512594/C
; Sequence 1512594, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reviolds, Angela
; APPLICANT: Reviolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Marshall, William
; APPLICANT: Scarling, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILER REFERENCE: 13499US
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Score 13.4; DB 1; Length 19;
Pred, No. 1.6e+02;
0; Mismatches 1; Indels
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i Sequence 1570074, Application US/11083784

i Sequence 1570074, Application US/11083784

j Publication No. US20050245475A1

i GENREAL INFORMATION:

i APPLICANT: Khvorova, Ansetasia

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

ITILE NOF INVENTION: Functional and Hyperfunctional siRNA

FILE REFERENCE: 14959US

CURRENT APPLICATION NUMBER: US/11/083,784

CURRENT APPLICATION NUMBER: 00/502,050

PRIOR APPLICATION NUMBER: 60/502,050

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2003-11-14

NUMBER: OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary

SEQ ID NO 1570074

TURDE: DATE: DATE: 2003-11-14

CONTARRED PROPRIETATION NUMBER: 60/426,137

PRIOR FILING DATE: 2003-11-14

SEQ ID NO 1570074
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Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 AAAGAGCCAGCGAAG 61
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; SEQ ID NO 1570062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1570062
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US-11-083-784-1570074
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US-11-083-784-1590808
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US-11-083-784-1560555

is Sequence 1560555, Application US/11083784

is Publication No. US20550245475A1

is GRNERAL INFORMATION:

is APPLICANT: Rivorova, Anastasia

APPLICANT: Rivorova, Anastasia

APPLICANT: Reynolds, Angela

APPLICANT: Reynolds, Angela

APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen

TILLE OF INVENTION: Punctional and Hyperfunctional siRNA

FILLE REPERENCE: 13499US

CURRENT FILLING DATE: 2003-018

PRIOR PILING DATE: 2003-010

PRIOR PILING DATE: 2003-11-14

NUMBER OF SEQ ID NUMBER: 60/426,137

SEQ ID NO 1560555

LENGTWARE: Proprietary

LENGTH. 10
                                                                                                                                                   Query Match 17.4%; Score 13.4; DB 1; Length 19; Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 12; Conservative 2; Mismatches 1; Indels
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sequence 1570.053

sequence 1570
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         ; ORGANISM: Homo sapiens
US-11-083-784-1522587
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; ORGANISM: Homo sapiens
US-11-083-784-1560555
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US-11-083-784-1570062
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Publication No. US2006000332A1
| Publication No. US2006000332A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: Uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 794222. Application US/10310914A

Sequence 79422. Application No. US2006000332A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Kwuzat
APPLICANT: Shiler, Kwuzat
TITLE OF INVENTION: uses thereof
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087-0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
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Pred. No. 1.8e+02;
3; Mismatches 3;
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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APPLICANT: Shiler, Kouzat
APPLICANT: Shiler, Kouzat
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       1 CCUCUGAGAGUGAAGGAG 18
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83.3%;
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Best Local Similarity 66.7%;
Matches 12; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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US-10-310-914A-794232
                                                                                                US-10-310-914A-721777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Human
US-10-310-914A-721777
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT APPLICATION NOWER: 12002-12-06
NUMBER OF SEQ ID NOS: 138402
SOFTWARE: Patentin version 3.3
SEQ ID NO 128513
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                                                                                                                                                                                                             Score 13.4; DB 1;
Pred. No. 1.6e+02;
3; Mismatches 1;
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Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-310-914A-128513/c
; Sequence 128513, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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1 Similarity 73.3%;
11; Conservative
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1590808
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                   GAAGCAGAUGUCCUG 16
                                                                                                                                                                                                                                                                                                           58 GAAGCTGATGTCCTG 72
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Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                   TYPE: RNA
CORGANISM: Homo sapiens
US-11-083-784-1590808
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserva
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Sequence 1213531, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SPELICANT:
APPLICANT:
Shiler, Kvuzat
TITLE OF INVENTION:
GENERAL APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1384402
SOFTWARE: Patentin version 3.3
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MIGHINGNICS, INC.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: APTES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.6%; Score 12.8; DB 1; Length 18; Best Local Similarity 87.5%; Pred. No. 2e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 1; Length 18;
Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 15896, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Forward Primer US-10-750-185-15896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.9%;
69.2%;
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6 CUCUGGAGUCCUC 18
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Best Local Similarity 69.2
Matches 9; Conservative
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US-10-750-623-15896/c
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LENGTH: 18
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Kvuzat

TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06007.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1288402

SOFTWARE: PARENTIN VERSION 3.3
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TITLE OF INVENTION: Baioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1268240
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                                                                                                                                                                         17.1%; Score 13.2; DB 1; Length 18; 77.8%; Pred. No. 1.8e+02; Live 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.2; DB 1; Length 18;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1268240, Application US/10310914A, Publication No. US20060003322A1, GENERAL INFORMATION:
APPLICANT: Benewich, Isaac
                                                                                                                                                                                                                                                                2 AAACAAGACGGCCTGGGG 19
                                                                                                                                                                                                                                                                                           1 AGACAGGAAGGCCUGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 ACTCTGGAATCCTATGGG 1
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NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 956449
                                                                                                                                                                           Query Match
Best Local Similarity 77.8
Matches 14; Conservative
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Best Local Similarity 83.3'
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Matches 15; Conservative
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US-10-310-914A-1268240/c
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US-10-310-914A-970022/c
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                                                                                                                                   US-10-310-914A-956449
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Human
                                                                                                             ORGANISM: Human
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LENGTH: 18
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US-10-310-914A-560230/C

Sequence 560230, Application US/10310914A

Sequence 560230, Application US/10310914A

Sequence 560230, Application US/10310914A

Sequence 560230, Application US/10310914A

SEQUENCE INVERTION: Use and TITLE OF INVERTION: Use thereof

TITLE OF INVERTION: Use US/10/310,914A

CURRENT APPLICATION VUMBER: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 560230

LENGTH: 18
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TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 537246
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Pred. No. 2e+02;
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                                                                                                                                                                                      16.6%; Score 12.8; DB 1; Length 18; 75.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 537246, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION: APPLICANT: Bentwich, ISaac
                        SOFTWARE: Patentin version 3.3 SEQ ID NO 319191
LENGTH: 18
                                                                                                                                                                                                                                                                                  37 TCTGAGAGGTAAAGAG 52
                                                                                                                                                                                                                                                                                                            3 UCUGAGAGGCACAGAG 18
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                                                                                                      Query Match
Best Local Similarity 75.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 TGGAGTCCTCTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.5
Matches 14; Conservative
    NUMBER OF SEQ ID NOS:
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US-10-310-914A-537246/c
                                                                                                                                           US-10-310-914A-319191
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                                                                                                TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Human
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Fourat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof

TITLE REPREBUCE: 066097.0200. CPUSOI;
CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

CURRENT FILING DATE: 2002-12-06

SOFTWARE: Patentin version 3.3

SEQUENT OF 199185
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US-10-314A-319191
US-10-310-914A-319191
Sequence 131914, Application US/10310914A
Sequence 131919, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Kruzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
TITLE OF EXPERENCE: 06097,0200,02001
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
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                                                                                      APPLICANT: HOLM, TOM
APPLICANT: BATES, Stephen
APPLICANT: RATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 15896
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Pred. No. 2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.6%; Score 12.8; DB 1; Length 18; Best Local Similarity 87.5%; Pred. No. 2e+02; Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Forward Primer US-10-750-623-15896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 GAGGTAAAGAGCCAGC 57
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                        DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
MMI GENOMICS, INC
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Best Local Similarity
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US-10-310-914A-198185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-198185
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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US-10-310-914A-919520/C
| Sequence 919520, Application US/10310914A
| Publication No. US20060003322A1
| GAPEALI INFORMATION:
| APPLICANT: Bentwich, Isaac
| APPLICANT: Bentwich, Isaac
| APPLICANT: Briler, Kvuzat
| TITLE OF INVENTION: Uses thereof
| TITLE OF INVENTION: USES TO SOURCE OF USO1
| TITLE OF INVENTION: USES TO SOURCE OF USO1
| TITLE OF USO1
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US-10-914A-815477

Sequence 815477, Application US/10310914A

SEQUENCE 815477, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Essac

APPLICANT: Bentwich, Essac

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

TITLE REPRENCE: 06097-0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 815477

LENGTH: 18
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1; Mismatches
                                                                                                                                                                                                                                         8; DB 1; Length 18; 2e+02;
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Pred. No. 2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                     Query Match
16.64; Score 12.8;
Best Local Similarity 81.24; Pred. No. 26-
Matches 13; Conservative 1; Mismatches
SOFTWARE: Patentin version 3.3
SEQ ID NO 78421
LENGTH: 18
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1 Similarity 87.5%;
14; Conservative
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Best Local Similarity 81.2%;
Matches 13; Conservative
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                      ORGANISM: Human
US-10-310-914A-784421
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ORGANISM: Human
                                                                                                          TYPE: RNA
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                                                                                                          Sequence 575025, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Value
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
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US-10-310-914A-784421

Sequence 784421, Application US/10310914A

Sequence 784421, Application US/10310914A

Sequence 784421, Application US/201010

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Batlac, Youzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REPRENEUES: 06087,0200,CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT PILING DAIR: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402
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Pred. No. 2e+02;
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62.5%;
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Best Local Similarity 62.5
Matches 10; Conservative
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Human
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RESULT 351

US-10-505-263-37/c

Sequence 37, Application US/10505263

Sequence 37, Application US/10505263

Publication No. US20060014940A1

GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Romero, Michael
ITILE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2

TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A1, and SLC26A2

TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2

TITLE OF INVENTION: WOMBER: US/10/505,263

CURRENT FILING DATE: 2004-08-20

PRIOR FILING DATE: 2003-02-28

PRIOR PRIOR FILING DATE: 2003-02-28

PRIOR PRIOR PLING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 96

SCOTTWARE: Patentin version 3.2

SEQ ID NO 37

LENGTH: 12

TUBE OF INVENTION NUMBER: PAT/USO3/06469

SEQ ID NO 37

LENGTH: 12

TUBE OF INVENTION NUMBER: PAT/USO3/06469
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Tasac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: uses thereof
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                                                                                                                                                      Score 12.8; DB 1; Length 18;
Pred. No. 2e+02;
1; Mismatches 2; Indels
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Pred. No. 2e+02;
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Best Local Similarity 81.2%;
Matches 13; Conservative
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Best Local Similarity 87.5'
Matches 14; Conservative
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Best Local Similarity
                                                                                                       US-10-310-914A-1353151
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                                                  TYPE: RNA
ORGANISM: Human
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SEQ ID NO 1353151
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  RESULT 347
US-10-310-914A-1087593
i Sequence 1087593, Application US/10310914A
i Publication No. US20060003322A1
i General Invorwarion:
APPLICANT: Bentwich, Isaac
i APPLICANT: Shiler, Kuuzat
i TITLE OF INVENTION: Uses thereof
i TITLE OF INVENTION: Uses thereof
i TITLE OF INVENTION: Uses thereof
i FILE REPREBRICE: 06087.0200. CPUSO1
i CURRENT APPLICATION NUMBER: US/10/310,914A
i CURRENT FILING DATE: 2002-12-06
i NUMBER OF SEQ ID NOS: 1388402
i SOFTWARE: Patentin version 3.3
i SEG ID NO 1087593
LENGTH: 18
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US-10-10-914A-1209729/C
US-10-10-914A-1209729/C
US-10-10-914A-1209729/C
US-10-10-914A-1209729 Application US/10310914A

Sequence 1209729 Application US/10310914A

PUBLICANT: Beltwich, Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION WUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PARCHILIN Version 3.3
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Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shiler, Kvuzat
TITUE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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US-10-310-914A-1353151
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LENGTH: 18
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0; Indels 0; Mismatches Matches 12; Conservative 8 GACGGCCTGGGG 19 |||||||||||| 12 GACGGCCTGGGG 1 & a

Search completed: April 19, 2006, 16:15:44 Job time : 1 secs

The Fago Light (uspid)

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Run on:

April 19, 2006, 16:06:39; Search time 0.001 Seconds (without alignments) 403.480 Million cell updates/sec

US-10-643-038-17\_994-1070 Title: Perfect score: Sequence:

1 caaacaagacggcctgggga.....gaagctgatgtcctgtcaag 77

Scoring table:

IDENTITY NUC Gapext 0.5

181 segs, 2620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 182 summaries

gedb:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	ACCESSION: A23021	ACCESSION: 123840	ACCESSION: AR074251	ACCESSION: AX032613	ACCESSION: BD185713	ACCESSION: BD089289	ACCESSION: AR228291	ACCESSION: CQ625286	ACCESSION: CQ625287	ACCESSION: AR466349	ACCESSION: AR466350	ACCESSION: AR085604	ACCESSION: CQ625284	ACCESSION: CQ625285	ACCESSION: AR466347	ACCESSION: AR466348	ACCESSION: AX649090	ACCESSION: CQ625288	ACCESSION: AR466351	ACCESSION: AX649091	ACCESSION: AX649092	ACCESSION: AX674032	ACCESSION: AX732023	ACCESSION: AX738057	ACCESSION: AX762421	ACCESSION: AR166421	ACCESSION: AR166424	ACCESSION: 119537	ACCESSION: 119540	ACCESSION: 186217	ACCESSION: 186220	ACCESSION: AR584728	ACCESSION: AX207952
SUMMARIES		ţ	10	A23021	123840	AR074251	AX032613	BD185713	BD089289	AR228291	CQ625286	CQ625287	AR466349	AR466350	AR085604	CQ625284	CQ625285	AR466347	AR466348	AX649090	CQ625288	AR466351	AX649091	AX649092	AX674032	AX732023	AX738057	AX762421	AR166421	AR166424	119537	I19540	186217	186220	AR584728	AX207952
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	ae (	Query	Match	36.6	36.6	27.3	27.3	20.0	19.2	19.2	18.7	18.7	18.7	18.7	18.7		18.2	18.2	18.2	17.9	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1
		1	score	28.2	28.2	21	21	15.4	4	14.8	14.4	14.4	14.4	14.4	14.4	14	14	14	-	13.8	13.4	13.4	13.4	13.4	13.4	13.4	13.4	ë.	ω.	ë.	13.2	ë.	•	•	13.2	13.2
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	AR466345 AR329584 AR329584 AR329584 AR362384 AR3629815 BD106403 I18626 AR455592 AR309596 AR455592 AR527981 AX527981 AX624831 AX624831 AX624831 AX63420 AX63420 AX63420 AR113242 AR113242 CS004712 CS004712	
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ACCESSION:AR397760 ACCESSION:AR658253 ACCESSION:AX813993		linear PAT 06-DEC-1994							^ ,	מאל			2001, mon to man securit				Grosveld, F.G. and				Length 33;	Indels 0; Gaps 0;				linear PAT 28-AUG-2000	
9.4 12.2 13 1 AR397760 9.4 12.2 13 1 AR658253 9.4 12.2 13 1 AX813993	ALIGNMENTS		ION A23021 M A23021.1 GI:833241 DS	synthetic construct NISM synthetic construct other sequences; artificial sequences.	1 (равев	L Patent: WO S	<pre>source 133 /organism="synthetic construct" /mol type="unassigned DNA"</pre>		cal Similarity 90.9%; Pred. No. 0.1;	GACGGCCTGGGGATACAACTCTGGAGTCCTCTG 40	GACGGCCTGGGGATACAACTCTGGAAGCTTCTG 1			123040 Sequence 4 from patent US 5538885. 173840		SM	Unclassified. 1 (bases 11 (bases Hollis, M. Needham, M.R.C., Gooding, C.,	Antoniou,M. Expression systems		source 155 /organism="unknown" /mol_type="unassigned DNA"	Match 36.6%; Score 28.2;	LOCAL SIMILARILY 90.9%; Fred. NO. 1es 30; Conservative 0; Mismatc	8 GACGGCCTGGGATACAACTCTGGAGTCCTCTG 40	33 GACGCCTGGGATACAACTCTGGAAGCTTCTG 1			ION AR074251. N AR074251.1 GI:10001006 DS .
180 C 181 182		RESULT 1 A23021/c LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL FEATURES	08	Š	Best Lo	, march	; A	1	RESULT 2 123840/c	DEFINITION	VERSION	SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL	2	Query	Best Lo Matches	È	q	RESULT 3	LOCUS	ACCESSION VERSION KEYWORDS
ACCESSION: AR270938 ACCESSION: AX016299 ACCESSION: AX152307 ACCESSION: BD022338	NOON		NOO	HHH	NOIS	NO	ACCESSION: BD229346 ACCESSION: BD222899 ACCESSION: 132082	NOIS	NO	NO	NOI	NOI	NOI	NOI	NO	NOIS		NOIS	NOI	1 11 11	NOI	NOIS	NOI	NOI	ACCESSION: AR029150 ACCESSION: AR02914	ONO	ACCESSION: COR28552 ACCESSION: AR212300 ACCESSION: AR285769
		AR403497 AR403497 AR069833 E15186												A K		88		SSS	X K	AX6 BD24	000	CSIC	X X X	AK7	ARO	ARI	
0000	) M 44 44 4	1 4 4 C C C	n w 4•	444	444	. 4 4	444	44.	***	* 4 4	44	কক	44.		1 - 1 - 1				нн.	440	00	N N C	100	N M	<b></b>		mmm
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ORGANISM

SOURCE

AUTHORS REFERENCE

source

TITLE JOURNAL FEATURES

RESULT 4
AX032613/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

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ORGANISM

SOURCE

REFERENCE AUTHORS

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12-WAR-2001 JP 2001068285
BIICHI SOBDA
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
OS Artificial Sequence
PN 47 20024696-A/14
PD 47-20025696-A/14
PD 47-20025696-A/14
PD 47-2002 JP 2002099422
PI RYDICHI KIYAWA, KEISUKE KITAJIMA, SHINOBU OGUCHI, MICHIO OISHI,
PI SAMU OHARA.
PI TAKAHIRO NAGASE
PC C12015/09, A61K31/711, A61K35/76, A61K38/00, A61F35/00,
PC C1201/68,
PC G1201/68,
PC G1201/68,
PC G1201/68,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method of arraying genome clone
Patent: JP 2001321190-A 1533 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
                                                                                                                                                                                                                                           A61K37/02
Description of Artificial Sequence:Synthetic DNA FH
Location/Qualifiers
Source
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Location/Qualifiers

1. .2

Acranism="synthetic construct"

/mol type="genomic DNA"

/db_xref="taxon:32630"
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/organism='Artificial Sequence'.
Location/Qualifiers
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20.0%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 1; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
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synthetic construct
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Application of KIAA0172 gene functions for therapeutics, diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kiyama,R., Kitalima,K., Oguchi,S., Olshi,M., Ohara,O. and Nagase,T. Application of KIAA0172 gene functions for therapeutics, diagnosis, and pharmaceuticals
Patent: JP 2002196596-A 14 24-DEC-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, INFO GENES CO LTD, KAZUSA DNA RESEARCH INSTITUTE
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                             Unclassified.

1 (bases 1 to 21)

Hanecak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
Imbach, J.Louis.
Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 59 14-SEP-1999;
Location/Qualifiers
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Myatt, J.R.
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Patent: BP 1015/15-8 59 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
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JP 2002369696-A/14.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 22)
                                                                                                                                                                                                                        /organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 59 from Patent BP1016715.
AX032613
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Best Local Similarity
Matches 21; Conserv
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AR466349
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Toftgard, M., Zaphiropoulos, P.G., Kogerman, P. and Grimm, T.
Molecules associated with the human suppressor of fused gene
Patent: US 6448020-A 3 10-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
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18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 1; Indels
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Sequence 10027 from Patent WO0192524.
CQ625287
CQ625287.1 GI:41675505
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Sequence 10026 from Patent W00192524.
                            DNA
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                          AR228291 21 bp
Sequence 3 from patent US 6448020.
AR228291
                                                                                                                                                                                                       1. .21
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/mol_type="genomic DNA"
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Location/Qualifiers
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CQ625286.1 GI:41675504
                                                                 AR228291.1 GI:27267057
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                                                                                                           Unknown.
Unclassified.
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Best Local Similarity
Matches 16; Conserv
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1 (bases 1 to 17)

Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 10027 03-FEB-2004;
Americham PLC; Buckinghamshire;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 10026 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                            Gu,Y., J1,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. Shannon,M.E. Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 10027 06-DEC-2001;
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18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 1; Indels
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AR466350.1 GI:42701407
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Sequence 10026 from patent US 6686188.
AR466349

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/organism="unknown"
/wol_type="genomic DNA"
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Location/Qualifiers
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                         Hominidae; Homo.
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AR466348 17 bp DNA Sequence 10025 from patent US 6686188. AR466348 GI:42701405
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Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Myosin-like gene expressed in human heart and muscle
Patent: WO 0192224-A 10024 06-DBC-2001;
Acomica, Inc. (US)
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Pred. No. 20;
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Cowsert, L. M.
Antisense modulation of G-alpha-13 expression
Patent: US 5981732-A 40 09-NOV-1999;
Location/Qualifiers
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Sequence 10024 from Patent WO0192524.
CQ625284.
CQ625284.1 GI:41675502
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                               AR085604 18 bp I
Sequence 40 from patent US 5981732.
AR085604
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Location/Qualifiers
               1. .17
/organism="unknown"
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Polynuclectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 10024 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX; Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Gaps Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and ö ö Shannon, M.E. Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 10025 06-DEC-2001; Query Match 18.2%; Score 14; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 20; Matches 14; Conservative 0; Mismatches 0; Indels linear ch 18.2%; Score 14; DB 1; Length 17; ll Similarity 100.0%; Pred. No. 20; 14; Conservative 0; Mismatches 0; Indels Sequence 10024 from patent US 6686188. AR466347 17 bp DN/ Sequence 10025 from Patent WO0192524. CQ625285 /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="taxon:9606" 1. .17 /organism="unknown" /mol\_type="genomic DNA" Inc. (US) Location/Qualifiers Location/Qualifiers CQ625285.1 GI:41675503 AR466347.1 GI:42701404 Homo sapiens (human) 3 reregaereeres 16 27 TCTGGAGTCCTCTG 40 27 TCTGGAGTCCTCTG 40 (bases 1 to 17) Hominidae, Homo. Query Match Best Local Similarity Unclassified.

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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.B.

Shannon,M.B.

Polymucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle predominantly in heart and muscle Amerena PLC; Buckinghamshire;

Amersham PLC; Buckinghamshire;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
Hominidae, Homo.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
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Shannon,M.E.
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Patent: EP 1273660-A 930 08-JAN-2003;
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Sequence 930 from Patent RP1273660.
AX649090
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/organism="unknown"
/mol_type="genomic DNA"
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Location/Qualifiers
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CQ625288.1 GI:41675506
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Shannon,M.E.
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Myosin-like gene expressed in human heart and muscle Patent: WO 0192524-A 10028 06-DEC-2001;
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17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 1; Indels
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Human sodium-hydrogen exchanger like protein 1
Patent: BP 1273660-A 931 08-JAN-2003;
Aeomica, Inc. (US)
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Sequence 10028 from patent US 6686188.
AR466351
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/db_xref="taxon:9606"

    .17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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/organism="unknown"
/wol_type="genomic DNA"
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Hominidae, Homo.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Patent: BP 1273660-A 932 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
Query Match 17.4%; Score 13.4; DB 1; Best Local Similarity 93.3%; Pred. No. 26; Matches 14; Conservative 0; Mismatches 1;
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Patent: WO 03004526-A 2477 16-JAN-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 2477 from Patent W003004526.
AX674032
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/db_xref="taxon:9606"
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il Similarity 93.3%;
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Best Local Similarity 93.33
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserva
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AX649092/c
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Patent: WO 0305177-A 3647 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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AX732023 17 bp DNA
Sequence 3657 from Patent WO03025175.
AX732023
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Best Local Similarity 93.3%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                      Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
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Mathur, E.J., Marsh, E.J. and Schoettlin, W.E.
Purified therametable pyrococcus furiosus DNA ligase
Patent: 18 6280998-A 14 28-AUG-2001;
Location/Qualifiers
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Mathur, B.J., March, B.J. and Schoettlin, W.E.
Purified thermostable pyrococcus furiosus DNA ligase
Patent: US 6280998-A 17 28-AUG-2001,
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 5742 from Patent WO03040369.
AX762421
AX762421.1 GI:32257037
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AR166421
AR166421.1 GI:16241735
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Sequence 17 from patent US 6280998.
AR166424
AR166424.1 GI:16241740
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/wol_type="unassigned DNA"
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                                                       Homo sapiens (human)
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Mathur, B.J., Marsh, B.J. and Schoettlin, W.B.
Purified thermostale Pyrococcus furiosus DNA ligase
Patent: Uso 5506137-A 14 09-APR-1996;
Location/Qualifiers
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Mathur, B.J., Marsh, B.J. and Schoettlin, W.E.
Purified thermostable Pyrococcus furiosus DNA ligase
Patent: 18 5506137-A 17 09-APR-1996;
Location/Qualifiers
                                                                         DB 1; Length 18;
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Sequence 14 from patent US 5506137.
119537
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Sequence 17 from patent US 5506137.
119540
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Pred. No. 29;
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/mol_type="unassigned DNA"
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/organism="unknown"
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/organism="unknown"
Location/Qualifiers
                                                                                                                                   18 GGATACAACTCTGGAGTC 35
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83.3%;
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Matches 15; Conservative
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Madison, B.L., Semple, J.B., Coombs, G.S., Reiner, J.E., Ong, B.O. and
Araldi, G.L.
Inhibitors of serine protease activity of matriptase or MTSP1
Patent: US 6797564-A 6 28-5EP-2004;
Dendreon San Diego LLC; Seattle, WA
Location/Qualifiers
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In Unassified.

In (Dasses 1 to 18)

Mathur, B. J., Marsh, B. J. and Schoettlin, W. B.

Purified thermostable pyrococcus furiousus DNA ligase
Purified thermostable pyrococcus furiousus DNA ligase

Location/Qualifiers

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Mathur, B.J., Marsh, B.J. and Schoettlin, W.B.
Purified thermostable pyrococcus furiousus DNA ligase
Patent: 18 5706672-A 17 23-DBC-1997;
Location/Qualifiers
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Sequence 14 from patent US 5700672.
186217
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Sequence 6 from patent US 6797504.
AR584728
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/organism="unknown"
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                                I86217.1 GI:3205935
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AR584728/c
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Madison, E.L., Ong, E.O. and Yeh, J.C.
Nucleic acid molecules encoding transmembrane serine proteases, the encoded proteins and methods based thereon coded proteins and methods based thereon CORVAS INTERNATIONAL, INC. (US)
Location/Qualifiers
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Ong, E.O. and Araldi, G.L.
Inhibitors of serine protease activity of matriptase or mtspl
Patent: WO 0220475-A 614-WAR-2002;
CORVAS INTERNATIONAL, INC. (US)
Location/Qualifiers
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Best Local Similarity 83.3%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 3; Indels
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    DB 1, Length 18;
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/mol_type="unassigned DNA"
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/noTe="0ligonucleoide Primer"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="caxon:32630"
/note="oligonucleoide primer"
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synthetic construct
other sequences; artificial sequences.
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  Score 13.2; D
Pred. No. 29;
0; Mismatches
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Sequence 6 from Patent W00220475.
AX473057
AX473057.1 GI:22207820
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Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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synthetic construct
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DEFINITION ACCESSION VERSION KEYWORDS

RESULT 35 CQ625283 LOCUS

ORGANISM

SOURCE

REFERENCE AUTHORS

source

FEATURES

JOURNAL

TITLE

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Gaps

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PAT 25-JUN-2003

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PAT 02-FEB-2004

RESULT 37
AX649089/C
LOCUS
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KEYWORDS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in tumoral suppression, tumoral suppression, apoptosis and/or viral resistance phenomena and their use as medicines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
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                                                                                                                                                                                                                                                                                                                                Length 17,
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Human sodium-hydrogen exchanger like protein 1
Patent: BP 1273660-A 929 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 5659 from Patent W003040369.
AX762338
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Sequence 10029 from Patent WO0192524.
CQ652889.1 GI:41675507
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Best Local Similarity 87.5%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches
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/db xref="taxon:9606"

    .17
    /organism="Homo sapiens"
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Location/Qualifiers
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Homo sapiens (human)
Homo sapiens
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Homo sapiens
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AX762338/c
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                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
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Shannon,M.E.
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Acomica, Inc. (US)
Location/Qualifiers
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                                                             CQ625283 17 bp DNA
Sequence 10023 from Patent W00192524.
CQ655283 GI:41675501
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Sequence 10023 from patent US 6686188.
AR466346
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Sequence 929 from Patent EP1273660.
AX649089.1 GI:29151907
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

ACCESSION VERSION

RESULT 36 AR466346 LOCUS

source

FEATURES

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AX649087.1 GI:29151905
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Best Local Similarity 92.9%;
Matches 13; Conservative
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                                           creekeccrcrek 17
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                    CTGGAGTCCTCTGA
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Shannon, M.B.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 10029 06-DEC-2001;
Acomica, Inc. (US)
Location/Qualifiers
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Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulio-Adamic, J., Sweedler, D. and Zinnen, S. Oligoribonucleotides with enzymatic activity Patent: US 6617438-A 816 09-SRP-2003; Sirna Therapeutics, Inc.; Boulder, CO
Location/Qualifiers
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                                                                                                                                             DB 1; Length 17;
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Pred. No. 38;
0; Mismatches 1; Indels
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Pred. No. 38;
0; Mismatches
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Sequence 816 from patent US 6617438.
AR398435
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Sequence 817 from patent US 6528640.
AR286445.1 GI:29724041

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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/mol_type="unassigned RNA"
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/mol_type="unassigned RNA"
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         PAT 20-PEB-2004
                                                                                                                                                      1 (bases 1 to 17)
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.B.
Polynucleotide encoding a human myosin-like polypeptide expressed
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Patent: BP 1273660-A 927 08-JAN-2003;
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17 bp DNA Sequence 10029 from patent US 6686188. AR466352. GI:42701409
                                                                                                                                                                                                                                 predominantly in heart and muscle.
Patent: US 668188-A 10029 03-FBB-2004;
Marcsham PLC; Buckinghamshire;
GBX;
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Pred. No. 38;
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Best Local Similarity 92.9%; Pred. No. 38;
Matches 13; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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AX649087
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/organism="unknown"
/mol_type="genomic DNA"
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                             Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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Human sodium-hydrogen exchanger like protein 1
Patent: BP 1273660-A 928 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: BP 1273660-A 933 08-JAN-2003;
Aeomica, Inc. (US)
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Sequence 316 from Patent WO03025177.
AX734726
                                                                                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Sequence 933 from Patent BP1273660.
AX649093
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/db_xref="taxon:9606"
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Pred. No. 38;
Sequence 928 from Patent EP1273660
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92.9%;
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BD203204.1 GI:33012974

JP 2002509721-A/6230.

Home sapiens (human)

SM Home sapiens (human)

Home sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

E 1 (bases 1 to 17)

S Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.

Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response

L Patent: JP 2002509721-A 6230 02-APR-2002;

RIBOZYME PHARMACEUTICALS INC
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24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOFT,
JAMES A MCSWIGGEN
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Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
BD201204
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Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptoesis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03021177-A 316 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           Score 12.4; DB 1; Length 17;
Pred. No. 38;
0; Mismatches 1; Indels
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participating in vasculogenic response
Key Location/Qualifiers
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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JP 2002509721-A/6230
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Best Local Similarity 92.9%;
Matches 13; Conservative
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RESULT 48 AX687578/c LOCUS

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REFERENCE AUTHORS

TITLE

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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                       Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                     Oligomeric compounds for the modulation of survivin expression Patent: WO 2004069991-A 113 19-AUG-2004; Santaris Pharma A/S (DK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 17)
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
                                                                                                                                                     Thrue, C.A., Petersen, K.D., Westergaard, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin-like gene expressed in human heart and muscle
Patent: WO 0192524-A 10022 06-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                Query Match 15.6%; Score 12; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 43; Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 10022 from patent US 6686188.
AR466345
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Sequence 10022 from Patent W00192524.
CQ625282.1 GI:41675500
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
   CQ858651.1 GI:51852618
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                                       Homo sapiens (human)
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Beet Local Similarity 100...
-has 12; Conservative
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                                                                                                                                                                       Wissenbach, M.
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                                                                                                                                                       Hansen, B.,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                 Shannon, M., Gu, Y. and Nguyen, C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus.
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Patent: WO 03025176-A 5066 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                         DNA
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CQ858651
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Sequence 5066 from Patent WO03025176.
AX727379
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Aeomica, Inc. (US)
Location/Qualiflers
                                                     AX687578 17 bp D
Sequence 310 from Patent BP1281758.
AX687578.1 GI:29410274
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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    .17
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PAT 18-SEP-2002
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                                                                                                                                                                                                                                                                                                                                     Transfer vectors and microorganisms containing human cytomegalovirus immediate-early promoter-regulatory DNA sequence Patent: US 5168062-A 13 01-DEC-1992; University of Iowa Research Foundation; Oakdale, IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        triple strand formation
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Local Similarity 86.7%; Pred. No. 46;
les 13; Conservative 0; Mismatches 2; Indels
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 86.7%; Pred. No. 46; ative 0; Mismatches
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Sequence 13 from patent US 5168062.
AR362385
AR362385.1 GI:34422358
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1 (bases 1 to 16)
Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA tr
Patent: US 5861244-A 4 19-JAN-1999;
Location/Qualifiers

    .16
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Seguence 4 from patent US 5861244.
AR029815.1 GI:5943029
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Novel LDL-receptor.
BD106403
BD106403.1 GI:23201221
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1 (bases 1 to 16)
Stinski, M.F.
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                  13; Conservative
                                                   63 TGATGTCCTGTCAAG
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AR362385/c
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Mayoro, P., McSWiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 556127-A 6986 20-MMY-2003;
Ribozyme Pharmecuticals, Inc. and Chiron Corporation; Boulder, CO Location/Qualifiers
             Polymuclectide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle Patent: US 6686188-A 10022 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
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                                                                                                                                                                                    15.6%; Score 12; DB 1; Length 17; 100.0%; Pred. No. 44; 0; Indels cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
/mol_type="unassigned RNA"
                                                                                                                      1. .17
/organism="unknown"
/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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Best Local Similarity 86.7%;
Matches 13; Conservative
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Stinski, M.F.
                                                                                                                                                                                                                       12; Conservative
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Best Local Similarity
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RESULT 54 AR362384/c LOCUS ORGANISM

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GI:31694802
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                                                         Unclassified.
     AR305492.1
                                                                                                                             Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
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                                                                   Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D., Hammond, H. and Hey, P.
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                                                                                                                                                                                                                                 DAVID COX,
DAVID GERHOLD, HOLLY HAMMOND, PATRICIA HEY
C12N15/12, C12N15/11, C12Q1/68, C07K14/705, C07K16/28, A61K38/17,
A61K39/395,
A61K48/00
                                                                                                                                                                                              PI
JP 2002501376-A/418.
Chlamydia sp.
Chlamydia sp.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
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                                                                                              Novel ibi-receptor
Patent: JP 2002501376-A 418 IS-JAN-2002;
THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST,
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1 (bases 1 to 16)
Spears, P.A.
Species-specific detection of Mycobacterium kansasii
Patent: US 5500341-A 12 19-MAR-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 16;
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15-ARR-1998 JP 1998543635
15-ARR-1997 US 60/043553,05-JUN-1997 US
ANDREW TODD,JOHN WILFRED HESS,CHARLES
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Sequence 450 from patent US 6545137.
AR305492
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Sequence 12 from patent US 5500341.
I18626
I18626.1 GI:1598981
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Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches
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/mol_type="unassigned DNA"

    .16
    /organism="Chlamydia sp."
/mol_type="genomic DNA"
/db_xref="taxon:35827"

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                                                                                                                                                     JP 2002501376-A/418
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Key
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                                                                                                                                                    PN JP 2002501376-A/PD JP 15-JAN-2002
PP 15-JAN-1999 JP 15-JAN-1997 US JOHN ANDREW TODD, JOHN THOWAS CASKEY, ROGER PI DAVID CGK, PI DAVID CRHOLD, HO C C T2N15/12, C12N15/PC A61K39/395, PC A61K49/00 CC Topology: Linear FH Key
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AR305492
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Unknown.
Unclassified.
1 (bases 1 to 16)
2 (bases 1 to 16)
2 Eang, L. and Markoff, L.
Replication-defective dengue viruses that are replication-defective in mosquitoes for use as vaccines
Patent: US 6685948-A 9 03-FEB-2004;
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Todd.J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
LDL-receptor
LDL-receptor
Patent: US 6555654-A 450 29-APR-2003;
The Wellcome Trust Limited as Trustee for the Wellcome Trust;
London;
1 (bases 1 to 16)
Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L.,
Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
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Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels
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Location/Qualifiers
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Sequence 450 from patent US 6555654.
AR309596.1 GI:31701601
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Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
The United States of America as represented by the Department of Health and Human Services; Washington, \mathrm{DC}_i
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Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.B., Michelotti, E.F., velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, W.Y. and Bruice, T.W.

Promoters for regulated gene expression
Patent: US 6838555-A 65 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
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                                                                                                                                                        Gaps
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                                                                                                                        14.5%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 58; 3; Indels ive 0; Mismatches 3; Indels
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    .16
    /organism="unknown"
    /mol_type="unassigned RNA"

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Sequence 65 from patent US 6838556.
AR630011
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Sequence 65 from Patent W00194600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
/mol_type="genomic DNA"
                                            Location/Qualifiers
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Best Local Similarity
Matches 13; Conserv
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Matches 13; Conserv
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KEYWORDS
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ORGANISM
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AR630011/c
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West Nile virus
Viruses; sRRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.
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Dengue viruses that are replication defective in mosquitos for use
as vaccines that are zeplication defective in mosquitos for use
Patent: WO 02074963-A 9 26-SEP-2002;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
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Oligomeric compounds for the modulation hif-lalpha expression
Patent: WO 03085110-A 67 16-OCT-2003;
Cureon A/S (DK)
Location/Qualifiers
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/mol type="unassigned DNA"
/mol type="unassigned DNA"
/mol type="staxon:32610"
/note="loscription of Artificial Sequence:antisense oligonucleotide to human HIF-la"
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14.5%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 58; 3; Indels ive 0; Mismatches 3; Indels
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Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="West Nile virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11082"
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AX927981
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Sequence 9 from Patent WO02074963.
AX552593
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                                                                                           38 CTGAGAGGTAAAGAGC 53
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Query Match
Best Local Similarity 81.2
Matches 13; Conservative
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Matches 13; Conserv
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Homo sapiens (human)
Homo sapiens
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                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                                                                                                                                                        Hofmann, K., Conradt, M. and Petersohn, D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 548 11-JUL-2002;
HENKEL KGAA (DB)
Location/Qualifiers
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Method for determining homeostasis of the skin
Petent: WO 02053774-A, 1872 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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AX624831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX632252 11 bp DNA Sequence 9294 from Patent WO02053774. AX632252 GI:28467867
                           11 bp D1
Sequence 548 from Patent WO02053773.
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/db_xref="taxon:9606"

    .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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                                                    AX470971
AX470971.1 GI:22206096
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                                                                                          Homo sapiens (human)
Homo sapiens
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Homo sapiens
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RESULT 66
AX470971/c
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AX624831/c
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AX632252/c
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Blatt, L., Mcswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Enzymatic nucleic acid treatment of diseases or conditions related
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                 Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 9294 11-JUL-2002; Henkel Kommanditgesellschaft auf Aktien (DE) Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                        14.3%; Score 11; DB 1;
100.0%; Pred. No. 48;
tive 0; Mismatches 0
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DANA FARBER CANCER INSTITUTE (US)
Location/Qualifiers

    .11
    /organism="Homo sapiens"
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/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Sequence 20 from Patent W00236761.
AX587244
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BD208921.1 GI:33018691
JP 2002512791-A/2511.
unidentified
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Gaps

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PAT 25-MAR-1994
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synthetic construct
synthetic construct
other sequences.

other sequences; artificial sequences.

l (bases 1 to 14)
Verrips,C.T., Maat,J., Edens,L. and Ledeboer,A.M.
Structural genes encoding the various allelic and maturation forms of preprochaumatin, recombinant cloning vehicles comprising said structural genes and expression thereof in transformed microbial host calls EP 005431-A 4 23-JUN-1982;
UNILEVER BV: UNILEVER PLC
Location/Qualifiers
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                                                                                                             Length 15;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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other sequences, artificial sequences.
1 (bases 1 to 15)
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                                                                                                            Query Match 14.3%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 60; Matches 11; Conservative 0; Mismatches

    .15
    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

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A15668/c
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to hepatitis C virus infection
RIGOZYME PHRAMACEUTICALS INC
RIGOZYME PHRAMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2511
PD 08-MAY-2002
PF 26-APR-1999 US 60/083217,18-SEP-1998 US 60/100842 PR 27-ARR-1999 US 60/083217,18-SEP-1999 US 60/100842 PR 27-REB-1999 US 09/274653 PI LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI PAVCO,
PI DENNIS MACEJAK
PC C12N9/00, AGIX31/7105, AGIX38/21, AGIK48/00, AGIP31/12, C12N15/09, PC C12N15/06
CC BRZYMATIC mucleic acid treatment of diseases or conditions CC
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Enzymatic nucleic acid treatment of diseases or conditions related
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Blatt, L., Mcswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Blatt, L., Mcswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Brymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
Patent: JP 2002512791-A 2512 08-MAY-2002;
RIBOZYMS FARAMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PD 08-MAY-2002
                                                                                                                                                                                                                  C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09, A61K37/66,
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C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
A61K37/66,
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PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR

25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI

LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
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/organism='Hepatitis virus (hepatitis C

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/organism='Hepatitis virus (hepatitis C

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related to
hepatitis C virus infection.
Location/Qualifiers
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100.0%; Pred. No. ...
0; Mismatches

    .15
    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

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BD208922
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JP 2002512791-A/2512.
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RESULT 74

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1 (bases I to 15)

E Blatt L., Mcswiggen, J.A., Roberts, B., Pavco, P.A. and Macejak, D.

E Blatt L., Mcswiggen, J.A., Roberts, B., Pavco, P.A. and Macejak, D.

E Brzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection

E Brzymatic nucleic acid treatment of diseases or conditions related to hepatitis V virus (hepatitis C virus)

E Brzymatic nucleic acid treatment of diseases or conditions of Hepatitis V virus)

E Brzymatic nucleic acid treatment of diseases or conditions CC Enzymatic nucleic acid treatment of diseases or conditions CC
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                                                                                                                                                                                                                                                                                                                                                                                Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.

Key
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14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels
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Sequence 2738 from Patent RP1502950.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
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CS004710.1 GI:58740065
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CS004710/c
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BD207153.1 GI:33016923
UP 2002512791-A/743.
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                                                                                                                                                                                                                                                                                                Unknown.
Unclassified.
Unclassified.
I (bases 1 to 15)
Draper, K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 5869253-A 186 09-FEB-1999;
Location/Qualifiers
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1 (bases 1 to 15)

2 Abaper, K.G.

Method and reagent for inhibiting hepatitis C virus replication
Patent: US 6132966-A 186 17-OCT-2000;
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Seguence 186 from patent US 6132966.
AR113242
   Best Local Similarity 85.7%; Pred. No. 64; Matches 12; Conservative 0; Mismatches
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                                                            S6 GCGAAGCTGATGTC 69
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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AUTHORS TITLE JOURNAL PEATURES

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ACCESSION VERSION KEYWORDS SOURCE

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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Unclassified.
Unclassified.
1 (bases 1 to 15)
1 sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
IL-5 targeted ribozymes
Patent: US 5616488-A 358 01-APR-1997;
Location/Qualifiers
                                                                                                                                                                                 Unclassified.
Unclassified.
1 (bases 1 to 15)
2 (bases 1 to 15)
2 (bases 2 to 15)
2 (bases 1 to 15)
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Draper,K.G.
Bnzymatic RNA molecule targeted against Hepatitis C virus
Patent: US 5610054-A 186 11-MAR-1997;
Location/Qualifiers
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Sequence 358 from patent US 5616488.
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Sequence 186 from patent US 5610054.
157649
15 bp Di
Sequence 357 from patent US 5616488.
139319
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Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches

    .15
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/wol_type="unassigned DNA"

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    /organism="unknown"
    /mol_type="unassigned DNA"

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                                                                                       I39319.1 GI:2083799
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Grlmm,S., Karpeisky,A., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
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Patent: RP 1820950-# 3340 02-REB-2005;
Ribozyme Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 2740 from Patent BP1502950.
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Sequence 3340 from Patent EP1502950.
CS005312
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CS004712.1 GI:58740067
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Best Local Similarity 85.7%;
Matches 12; Conservative
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RESULT 79 CS005312 LOCUS DEFINITION

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                                                                                                                                                                                              Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpelsky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, Pavco, P., Beigelman, L., Sullivan, S.W., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
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                        AX635601 15 bp RNA Sequence 2740 from Patent BP1260586. AX635601
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/db xref="taxon:32644"
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Best Local Similarity 85.7%;
Matches 12; Conservative
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Patent: US 5658780-A 373 19-AUG-1997;
Location/Qualifiers
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                        15 bp DN Sequence 373 from patent US 5658780.
    ; Score 10.8; DE; Pred. No. 64; 0; Mismatches
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Sequence 2738 from Patent BP1260586.
AX635599

    .15
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RESULT 84
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PAT 29-SEP-1999

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Seguence 4 from Patent WO0066780.
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PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN, NICHOLAS MUZYCZKA, WILLIAM W HAUSWIRTH PI CHRISTLAN TESCHENDORF,
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JP 2002542805-A/4.
synthetic construct
synthetic construct
other sequences; artificial sequences.
1 (Dases 1 to 13)
Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
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PC C12N15/09, A01K67/027, C12N9/00, C12Q1/68, C12N15/00 of C12N15/00 of Artificial Sequence: SYNTHETIC PEPTIDE Location/Qualifiers
                                                                  Unclassified.

1 (bases 1 to 13)

Brzezinski,R., Dery,C.V. and Beaulieu,C.
Thermostable xylanase DNA, protein and methods of use Patent: Uccation/Qualifiers
                                                                                                                                                                                                         13.5%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 68; 1; Indels tive 0; Mismatches 1; Indels
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        'organism="synthetic construct"
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UNIVERSITY OF FLORIDA
OS Artificial Sequence
PN JP 2002542805-A/4
PD 17-DEC-2002
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/organism="unknown"
/mol_type="unassigned DNA"
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I (base 1 to 14)

E latt, L., Meswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection

A HEDOZYME PHARMACEUTICALS INC
OS HEPATLIST virus (hepatitis C virus)
PR 2002512791-A/2866
PD 08-MAY-2002
PP 26-APR-1999 JP 2000545991
PR 27-APR-1999 US 60/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI
LAMRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
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CI2N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
A61K37/66,
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'organism='Hepatitis virus (hepatitis C
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13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                 synthetic construct
synthetic construct
other sequences; artificial sequences.
                                                                                                                                                                                                                                                    Patent: WO 0066780-A 4 09-NOV-2000;
University of Florida (US)
Location/Qualifiers
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/mol_type="unassigned RNA"
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/note="SYNTHETIC PEPTIDE"
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JP 2002512791-A/2866.
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AX048268.1 GI:11877033
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PAT 26-JAN-2000

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AUTHORS TITLE JOURNAL

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REFERENCE

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FRATURES

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Unclassified.

1 (bases 1 to 10)

Austin,R.C., Hirsh,J. and Weitz,J.I.

Methods and compositions for diagnosis of hyperhomocysteinemia

Patent: US 5817461-A 4 06-OCT-1998;

Location/Qualifiers

1.10
                                                                                                                                                               Roberts, J.A. and Paul, W.
CONTROL OF PLANT ABSCISSION AND POD DEHISCENCE OR SHATTER
PATENT: WO 991580-A 4 01-APR-1999;
BIOGEMMA UK LIMITED (GB); ROBERTS JEREMY ALAN (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 10)

2 Smith,H.S. and Chen,L.-C.
Methods for identifying genes amplified in cancer cells
Patent: US 5776683-A 14 07-JUL-1998;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels
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Sequence 14 from patent US 5776683.
AR016246.1 GI:3972523
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Sequence 4 from patent US 5817461.
AR044027
AR044027.1 GI:5965492
             10 bp
Sequence 4 from Patent WO9915680.
A97598
A97598.1 GI:6780901
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1 (bases 1 to 10)
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Matches 10; Conservative
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Nees, M. and Duerst, M.
DNA FOR WALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
Patent: WO 982375-A 3 04-JUN-1998;
DRUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
LOCATION/Qualifiers
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Regulated genes by stimulation of chondrocytes with IL-lbeta Patent: BY 0705842-A 64 10-APR-1996;
HORGHST AG (DB)
Other publication ZA 9508381 960424
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
Location/Qualifiers
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 Pred. No. 71;
0; Mismatches

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Sequence 64 from Patent BP0705842.
A52274.
A52274.1 GI:2852038
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Sequence 3 from Patent WO9823775.
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 Best Local Similarity 91.7%;
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A91804.1 GI:6740684
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3 I (bases 1 to 10)
S Tam,S.-Y., Tsai,M. and Galli,S.J.
Rin2, a novel inhibitor of Ras-mediated signaling
All Patent: US 5965707-A 3 12-0CT-1999;
Location/Qualifiers
                                   ch 13.0%; Score 10; DB 1; Length 10; Similarity 100.0%; Pred. No. 66; 10; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 10)
Pardee,A.B. and Liang,P.
System for comparing levels or amounts of mRNAs
Patent: US 5965409-A 13 12-OCT-1999;
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Sequence 28 from patent US 6077948.
AR099718
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Sequence 13 from patent US 5965409.
AR079092
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Sequence 3 from patent US 5965707.
AR079528
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Novel microsatellite DNA derived from pear plants and method for discriminating pear plants using the same.
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1 (bases 1 to 10)
Russell,M.E. and Utans,U.
Mediators of chronic allograft rejection (AIF-1) and DNA encoding
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1 (bases 1 to 10)

Austin, R. C., Hirsh, J. and Weitz, J.I.

Methods and compositions for diagnosis of hyperhomocysteinemia

Patent: US 6132965-A 4 17-OCT-2000;

Location/Qualifiers
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Location/Qualifiers
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AR113051 GI:14093373
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21-JUL-2000 JP 2000220339
TOSHIYA YAMAMOTO, YUTAKA SAWAMURA, TSUYOSHI IMAI, NAGAO MAISUDA, TOSHIHRO SALTO, MORIYUKI SHODA, KAZUO KOTOBUKI, KENKI HAYASHI, YOSHIYUKI BAN, MASANORI KOZONO, TETSUYA KIMURA C12Q1/68, A01H1/00, C12N15/09, C12N15/00
Description of Artificial Sequence:Primer Location/Qualifiers
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Roberts, B.L. and Shankara, S. Roberts, B.L. and Shankara, S. Perparation and use of superior vaccines Patent: JP 2002534056-A 2115 15-OCT-2002;
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    /organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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JP 2002534056-A/2115
15-OCT-2002
18-JUN-1999 JP 2000554749
19-JUN-1998 US 60/090039
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JP 2002534056-A/2115.
Homo sapiens (human)
Homo sapiens
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Unclassified.
1 (bases 1 to 10)
Kussell, M. B. and Utans, U.
Mediators of chronic allograft rejection and DNA molecules encoding
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                                                                                                                                                   Length 10
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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66;
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100.0%; Pred. No. 66;
tive 0; Mismatches
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Patent: US 5527884-A 28 18-JUN-1996;
Location/Qualifiers
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Sequence 28 from patent US 5527884.
122447.1 GI:1602801
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="unknown"
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BD248338.1 GI:33058108
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Best Local Similarity 100.
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PAT 10-APR-2003

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1 (bases 1 to 10)
Romick,T.L. and Praser,M.S.
Romick,T.L. and Praser,M.S.
PCR techniques for detecting microbial contaminants in foodstuffs
Patent: 10S 6469743-A 132 22-OCT-2002;
ConAgra Grocery Products Company; Fullerton, CA
Location/Qualifiers
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Tamps.-Y. Tsai,M. and Galli,S.J.

Rinz, a novel inhibitor of Ras-mediated signaling

Patent: US 6500942-A 3 31-DEC-2002;

Beth Israel Deaconess Medical Center and The Board of Trustees of the Leland Stanford, Yr. University; Palo Alto, CA

Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 3 from patent US 6500942.
AR270938
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Sequence 2 from Patent W09949046.
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/organism="unknown"
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/mol_type="genomic DNA"
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Matches 10; Conservative 0
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1 (bases 1 to 10)
Liang, P., Pardee, A.B. and Bianchi, C.F.
Method of differential display of exposed mRNA by RT/PCR
Patent: US 5599672-A 13 04-FEB-1997;
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llarity 100.0%; Pred. No. 66;
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Sequence 132 from patent US 6468743.
AR238724 1 GI:27283794
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Sequence 13 from patent US 5599672.
134793
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Sequence 13 from patent US 5665547.
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/wol_type="unassigned DNA"
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Unclassified.
1 (bases 1 to 10)
Pardee, A.B. and Liang, P.
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                                                             Conservative
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PAT 07-SEP-2000

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Location/Qualifiers
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Unclassified.
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DNA for evaluating progress potential of cervical diseases.
BD023238
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Patent: JP 2001504703-A 3 10-APR-2001;
DEUTSCHES KREBSPORSCHUNGSZENTRUM STIFTUNG DES BFFENTLICHEN RECHTS
PN 10-APR-2001
PP 12-NOV-1997 JP 1998524127
PR 27-NOV-1996 DE 19549207.6
PI MATHIAB DIRUST, MATHIAB NESS
PC CLANIS/09, CO7KI4/00, CO7KI6/00, C12P21/02, C12Q1/68, C12Q1/70, PC
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JP 2001504703-A/3.
Homo sapiens (human)
Homo sapiens
Mammalia; Butheria; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 10)
Durust, M. and Ness, M.
                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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                                           13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 66; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                            linear
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Patent: WO 0138577-A 222 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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                                                                                                                                                                                                            DNA
                                                                                                                                                                                                       Sequence 222 from Patent W00138577. AXIS2307

    .10
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

/db_xref="taxon:32630"
/note="Arbitrary primer A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C12N15/00
Strandedness: Single;
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/desc = 'Primer'
Key Lo
                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                         Query Match 13.0
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                      51 AGCCAGCGAA 60
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Matches 10; Conserva
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AX152307/c
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BD023238
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1 (bases 1 to 14)
Milliman,C.L.

Mulliman,C.L.

Patent: US 5830654-A 2 03-NOV-1998;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 13)
Gaudernack, G., Eriksen, J.A. and Moller, M.
Immunogenic . Deta. - amyloid peptide
Batent: US 6861057-A 14 01-MAR-2005;
GemVax AS; Oslo;
NOX;
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13.0%; Score 10; DB 1
Best Local Similarity 100.0%; Pred. No. 79;
Matches 10; Conservative 0; Mismatches
                                                                                     Query Match 13.0%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 66; Matches 10; Conservative 0; Mismatches
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Sequence 14 from patent US 6861057.
AR641426
AR641426.1 GI:62776633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
/wol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR051174 14 bp
Sequence 2 from patent US 5830654.
AR051174 GI:5974538
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .13
/organism="unknown"
/mol_type="genomic DNA"
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Unknown.
Unclassified.
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I15960/c
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BD197865.
BD197865.
BURATYOL1-A/891.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

TE (bases 1 to 14)

Revoc, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
TREOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/891
PD 02-ARR-1099 JP 2000541291
PR 24-MAR-1999 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
                                                                                                                                                                                                                                                                                                                                                                                                              ပ္ပ
                  BD068997 14 bp RNA linear PAT 27-AUG-2002 Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD197865 14 bp RNA linear PAT 17-JUL-2003 weelhod and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
BD197865
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JP 2002509721-A/891
02-APR-2002
24-MAR-1999 UF 2000541291
27-MAR-1999 US 60/079678
PAMMELA PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT, JAMES A MCSWIGGEN
                                                                                                                                                                1 (bases 1 to 14)
Akhtar, S., Fell, P. and Mcswiggen, J.A.
Brzymatic nucleic acid treatment of diseases or conditions related
to level epidermal growth factor receptors
Patent: JP 2001511003-A 1837 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC, ASTON UNIV
                                                                                                                                                                                                                                                                                                                                                                                       Topology: Linear:
Enzymatic nucleic acid treatment of diseases or conditions
related to
levels of epidermal growth factor receptors
Key
Location/Qualiflers
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                                                                                                                                                                                                                                                           Unidentified
JP 2001511003-A/1837
07-AUG-2001
31-JAN-1999 UP 1998532913
31-JAN-1997 US 60/036476,04-DEC-1997 US
IR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Unidentified'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
82;
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/db_xref="taxon:32644"
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                                                                                BD068997.1 GI:22614600
JP 2001511003-A/1837.
unidentified
unidentified
unclassified.
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Matches 10; Conserva
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BD197865/c
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A61P29/00,
°C A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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Bazymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors

Patent: US 6623962-A 1837 23-58P-2003;

Sirna Therapeutics, Inc. and Aston University; Boulder, CO

Location/Qualifiers
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
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82;
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Milliman,C.L.
Milliman,C.L.
Milliman,C.L.
Patchic acid probes to Haemophilus influenzae
Patent: US 5472843-A 2 05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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82;
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/wol_type="unassigned DNA"
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Sequence 2 from patent US 5472843.
115960
                                                                                                                                                                                                                              1. .14
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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/organism="unknown"
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Best Local Similarity 100.
Matches 10; Conservative
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Unclassified.
1 (bases it old)
Harris, L. J., Lipsich, L.A. and Walls, M.A.
Harris, L.J., Lipsich, L.A. and Walls, M.A.
Human immunoglobulines produced by recombinant DNA techniques
Patent: BP 0314161-A1 2 03-WAY-1989;
Location/Qualifiers
                                                                                              Score 9.8; DB 1; Length 13; Pred. No. 85; 0; Mismatches 2; Indels
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2 from Patent BP 0314161.
  /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Sequence 1247 from patent
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Best Local Similarity 84.6%;
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Matches 11; Conservative
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AR027402/c
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.51 - specific sequence in 18S rRNA gene.
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03-JUN-1996 JP 96P 140087
YAMAGISHI WASAHIRO, TAKAI YUKIE, MIKAWA TAKASHI, OOHARA AKIKO,
HARA MARI,
UEDA MAKOTO
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1 (bases 1 to 13)

1 (bases 1 to 13)

Ramadishi, M., Takai, Y., Mikawa, T., Oohara, A., Hara, M. and Ueda, M. PRODUCTION OF (8)-GAMMA-HALOGENATED-BETA-HYDROXYLACTIC ACID ESTER PATENT: JP 1998052290-A 19 24-FEB-1998;
MITSUBISHI CHEM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown.
Unknown.
Unclassified.
1 (bases 1 to 13)
Yamagishi,M., Takai,Y., Mikawa,T., Hara,M., Ueda,M. and Ohara,A.
Method for producing ester of
(S)-.gamma.halogenated-.beta.-hydroxybutyric acid
(S)-.gamme.halogenated-.beta.-hydroxybutyric acid
Patent: US 581685-A 49 06-APR-1999;
Location/Qualifiers
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/organism='Selenophoma donacis' FT
/strain='CBS417.51'.
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                                            DB 1; Length 14;
82;
                                                                                              0; Indels
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Pred. No. 85;
0; Mismatches
                                          13.0%; Score 10; DB 100.0%; Pred. No. 82; tive 0; Mismatches
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Sequence 49 from patent US 5891685,
AR069833
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strandedness: Double;
/mol_type="genomic DNA"
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Selenophoma donacis CBS417.51
R15186
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JP 1998052290-A/19
24-FEB-1998
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l Similarity 84.6%;
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JP 1998052290-A/19.
                             Query Match
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13 AGCTGATGACTTG 1
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Query Match Best Local S: Matches 11

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Unclassified.
1 (bases 1 to 14)
1 (bases 1 and Beck, J.J.
Defection of fungal pathogens using the polymerase chain reaction
Patent: US 5955274-A 26 21-SEP-1999;
Patent: US 5955274-A 26 21-SEP-1999;
                                                                                                                                                                                                                                                        Unclassified.
Unclassified.
1 (bases 1 to 14)
Eck, J. Joseph.
Detection of fungal pathogens using the polymerase chain reaction
Patent: US 5814453-A 26 29-SEP-1998;
Location/Qualifiers
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Sequence 26 from patent US 5955274.
AR074642.1 GI:10001395
    Pred. No. 89;
0; Mismatches
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Sequence 26 from patent US 5814453.
AR043142
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/organism="unknown"
/mol_type="unassigned DNA"
Best Local Similarity 84.6%; Pred. No.
Matches 11; Conservative 0; Mismatc
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Best Local Similarity 84.6%;
Matches 11; Conservative
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                  11; Conservative
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84.6%; Pred. No. 89;
ive 0; Mismatches 2; Indels
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                                                                                                           1 (bases 1 to 14)
Hampel,A.B., Tritz,R.H. and Hicks,M.F.
Hairpin ribozymes
Patent: US 5856188-A 62 05-JAN-1999;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 14)

Hampel, A.E. and Tritz, R.H.

HIV targeted ribozymes

Patent: US 5858785-A 62 12-JAN-1999;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 14)
Hampel,A.E., Tritz,R.H. and Hicks,M.
HIV targeted hairpin ribozymes
Patent: US 5869339-A 62 09-FEB-1999;
Location/Qualifiers
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Sequence 62 from patent US 5869339.
AR034393.1 GI:5949998

    .14
    /organism="unknown"
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
    Sequence 62 from patent US 5856188.
AR027402
AR027402.1 GI:5938222
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14 AAACAGGACGGTC 2
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AR028856/c
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REFERENCE AUTHORS

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34 TCCTCTGAGAGGT
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Keating, M.T., Sanguinetti, M.C. and Splawski, I.
Mutations in the KCNE1 gene encoding human mink which cause
arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
Patent: US 6274332-A 99 14-AUG-2001;
Location/Qualifiers
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Draper.K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and
Thompson, J.D.
Method and reagent for inhibiting human immunodeficiency virus
                                                                                                                                                                                  Gaps
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          1 (bases 1 to 14)
Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Thompson, J.D.
HIV nef targeted ribozymes
Patent: US 5972704-A 49 26-OCT-1999;
Location/Qualifiers
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Pred. No. 89;
0; Mismatches

    .14
    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 49 from patent US 6159692.
AR120747.1 GI:14104323
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Sequence 99 from patent US 6274332.
AR164788
AR164788.1 GI:16237972
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/mol_type="unassigned DNA"
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1 Similarity 84.6%;
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AR120747/c
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S JP 2001511003-A/1769.

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Unclassified.

CB I (bases 1 to 14)

BACHARA S., Fell, P. and Mcswiggen, J.A.

Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

AL EACTOR TECHNOLOGY 07-AUG-2001;

RIBOZYME PHARMACEUTICALS INC, ASTON UNIV

BY 14-JAN-1999 UP 1998532913

PF 14-JAN-1999 US 60/036476, 04-DEC-1997 US 08/985162 PI SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC C12N9/00, C07XL4/71

CC Strandedness: Single;

CC Strandedness: Single;

CC ENZYMALG nucleic acid treatment of diseases or conditions CC
                                                                                                                                                                            Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
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Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
RIBOZYME PHARWACEUTICALS INC
OS HEPATITIS UNIUS (hepatitis C virus)
PN JP 2002512791-A/2936
PD 08-MAY-2002
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Enzymatic nucleic acid treatment of diseases or conditions
related to
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Key
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Location/Qualifiers
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/mol_type="genomic RNA"
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BD209346.1 GI:33019116
JP 2002512791-A/2936.
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Unclassified.
1 (bases 1 to 14)
Ligon.J.M. and Beck,J.J.
Detection of fungal pathogens using the polymerase chain reaction
Patent: US 5585236-A 26 17-DEC-1996;
Patent: US 5585236-A 26 17-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 14)
Draper, K.G., Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Thompson, J.D.
HIV targeted ribozymes
Patent: US 569335-A 49 02-DEC-1997;
Location/Qualifiers
                                                                                                                              Length 14;
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Best Local Similarity 84.6%; Pred. No. 89;
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Best Local Similarity 84.6%; Pred. No. 89;
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Sequence 49 from patent US 5693535.
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Sequence 24 from patent US 6333152.
AR179956
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Sequence 26 from patent US 5585238.
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/mol_type="unassigned DNA"
                                                                                            /db_xref="taxon:9606"
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nilarity 84.6%;
Conservative 0
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PF 26-APR-1999 JP 2000545991

PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR 25-EB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI PAVCO,

PI DENNIS MACEJAK

PC C12N9/00,A61K31/7105,A61K38/21,A61K4°''

PC C12N15/00

CC Enverse
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                                                                                                                                                                          DENNIS MACEJAK
C12N9/00, AGIK31/7105, AGIK38/21, AGIK48/00, AGIP31/12, C12N15/09,
AGIK37/66,
C12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 14)

Keating, M.T., Sanguinetti, M.C., Karan, M.E., Landes, G.M.,

Connors, T.D., Burn, T.C. and Splawski, I.

KVLQTI-QT extension syndrome
Patent: JP 2002221045-A 97 16-JUL-2002;

UNIVERSITY OF UTAH REGRARCH FOUNDATION, GENZYMB CORP

EN JP 2002521045-A/97

PD 16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PI TIMOTHY D CONNORS, TIMOTHY C BURN, IGOR SPLAWSKI PC C12N15/09, A01K67/027, C07K14/46, C07K14/47, C07K16/18, C12N1/15, PC C12N1/19,
                                                                                                                                                                                                                                             \mathtt{Enzymatic} nucleic acid treatment of diseases or conditions related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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PR 29-JUL-1998 US 60/094477,17-AUG-1998 US 09/135010
MARK T KEATING,MICHAEL C SANGUINETTI,MARK E KARAN,GREGORY M

    .14
/organism='Hepatitis virus (hepatitis C

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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Key Location/Qualifiers
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84.6%; Pred. No. 89;

    .14
    /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

    .14
    /organism="Homo sapiens"
/mol_type="genomic DNA"

                                                                                                                                                                                                                                                                             hepatitis C virus infection.
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BD222899
BD222899.1 GI:33032669
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Homo sapiens (human)
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BD222899
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/mol_type="genomic DNA"
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                             Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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JOURNAL
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Keating, M.T., Sanguinetti, M.C. and Splawski, I.
Mutations in the KCNE1 gene encoding human mink which cause
arrhythmia susceptiability thereby establishing KCNE1 as an LQT gene
Patent: US 6432644-A 99 13-AUG-2002;
University of Utah Research Poundation; Salt Lake City, UT
Location/Qualifiers
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Reating, M.T., Sanguinetti, M.C., Curran, M.E., Landes, G.M.,
Connors, T.D., Burn, T.C. and Splawski, I.
KVLQTI--a long qt syndrome gene
Patent: US 6420124-A 39 16-JUL-2002;
University of Utah Research Foundation and Genzyme Corporation;
Salt Lake City, UT
Location/Qualifiers
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                                                                   1 (bases 1 to 14)

Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W. Gene expression profiles in normal and cancer cells Patent: US 6333152-A 24 25-DBC-2001;
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AR223166.1 GI:23331019
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Sequence 99 from patent US 6420124.
AR218751
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0; Mismatches
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/organism="unknown"
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/organism="unknown"
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 GI:20221989
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12.7%;
Best Local Similarity 84.6%;
Matches 11; Conservative
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                                        Unknown.
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FEATURES
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AUTHORS
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JOURNAL
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AUTHORS
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Keating, M.T., Sanguinetti, M.C. and Splawski, I.
Keating, M.T., Sanguinetti, M.C. and Splawski, I.
Mutations in the KCNE1 gene encoding human mink which cause
arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
Patent: US 6323026-A 99 27-NOV-2001;
University of Utah Research Foundation; Salt Lake City, UT
Location/Qualifiers
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Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
KYLATI--a long OT syndrome gene
Patent: US 6451534-A 99 17-SEP-2002;
University of Utah Research Foundation and Genzyme Corporation;
Salt Lake City, UT
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DB 1; Length 14;
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Pred. No. 89;
0; Mismatches 2; Indels
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                                      0; Mismatches
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AR229928
Score 9.8; Di
Pred. No. 89;
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0; Mismatches
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Sequence 99 from patent US 6323026.
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/organism="unknown"
/mol_type="genomic DNA"
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    14
    organism="unknown"

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BD000925
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ACCESSION
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KEYWORDS
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DEFINITION
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BD000925/c
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KEYWORDS
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                                                                                                                 1 (bases I to 14)
Keating, M.T., Sanguinetti, M.C., Curran, M.E., Landes, G.M.,
Connors, T.D., Burn, T.C. and Splawski, I.
Diagnostic method for KVLQT1--a long QT syndrome gene
Patent: US 6582913-A 99 24-UN-2003;
University of Utah Research Foundation and Genzyme, Inc.; Salt Lake
City, UT
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              PAT 17-AUG-2003
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Rarymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors

Patent: US 6623962-A 1769 23-SEP-2003;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  Query Match 12.7%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 89; Matches 11; Conservative 0; Mismatches 2; Indels
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Sequence 1769 from patent US 6623962.
AR403429
AR403429.1 GI:40150879
             AR344622 14 bp I
Sequence 99 from patent US 6582913.
AR344622
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Sequence 44 from Patent W00224950.
AX467015
                                                                                                                                                                                                                                               1. .14
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                                                        AR344622.1 GI:33740691
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synthetic construct
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Unclassified.
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Matches 11; Conserv
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AX467015/c
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DEFINITION
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ACCESSION
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AR403429
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Holesek, J.J. and Mamone, A.J.
Holesek, J.J. and Maysejak, D.G.
Holesek, J.J. and Mayse
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="Synthetically generated oligonucleotide"
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Human immunodeficiency virus
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
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Method and reagent for inhibiting HBV viral replication Patent: BP 1288296-A 84 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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Pred. No. 89;
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 14)
Patent: WO 0224950-A 44 28-MAR-2002;
Neuromics Inc. (US)
Location/Qualifiers
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Sequence 84 from Patent EP1288296.
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Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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JP 2000342285-A/85.
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CI2N15/09, CI2N5/10, CI2N1/00, CI2N9/22//(CI2N5/10, CI2R1:91), PC
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07/882824 PR
07/882821 PR
07/883823 PR
07/884073 PR
07/884313 PR
07/88431 PR
07/884431 PR
07/88451 PR
07/98859 PR
07/948359 PR
07/948359 PR
07/987133 PI
GEN, PI DENNIS G
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           07/882821 PR
07/882221 PR
07/884232 PR
07/884333 PR
07/884331 PR
07/884521 PR
07/935854 PR
07/948359 PR
07/948359 PR
07/9871229 PR
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other sequences; artificial sequences.

1 (bases 1 to 14)
Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J. and Manone, A.J.
Method and reagent for inhibiting viral replication
Patent: JP 2000142286-A 85 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2000142286-A/85
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921
14-MAY-1992 US 07/882892,14-MAY-1992 US 07/883823
14-MAY-1992 US 07/88349,14-MAY-1992 US 07/884407
14-MAY-1992 US 07/884474,14-MAY-1992 US 07/884431
14-MAY-1992 US 07/884432,14-MAY-1992 US 07/884431
14-MAY-1992 US 07/884432,14-MAY-1992 US 07/884521
31-UUL-1992 US 07/93436,14-MAY-1992 US 07/935854
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359
15-CCT-1992 US 07/95132,07-DEC-1992 US 07/948359
07-DEC-1992 US 07/95132,07-DEC-1992 US 07/987129
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14-MAY-1992 US 07/88286,14-MAY-1992 US 07/882814

14-MAY-1992 US 07/88286,14-MAY-1992 US 07/882818

14-MAY-1992 US 07/882892,14-MAY-1992 US 07/882818

14-MAY-1992 US 07/882892,14-MAY-1992 US 07/882818

14-MAY-1992 US 07/882921,14-MAY-1992 US 07/884073

14-MAY-1992 US 07/884436,14-MAY-1992 US 07/88431

14-MAY-1992 US 07/884436,14-MAY-1992 US 07/88451

14-MAY-1992 US 07/884436,14-MAY-1992 US 07/88451

15-071-1992 US 07/984436,14-MAY-1992 US 07/88451

15-071-1992 US 07/98132,07-DEC-1992 US 07/948359

15-071-1992 US 07/98132,07-DEC-1992 US 07/98135864

07/98132,07-DEC-1992 US 07/98132,07-DEC-1992 US 07/98135864

07/98132,07-DEC-1992 US 07/981318

07/98132,07-DEC-1992 US 07/981318
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Location/Qualifiers
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-01-MAY-2000 JP 2000132651
11-MAY-1992 US 07/882689,14-MAY-1992

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BD001354.1 GI:18625913
JP 2000342286-A/85.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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DEFINITION
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VERSION
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BD001354/c
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1. .14
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/note="MHC-DRB pseudogene"
                                                   C AGIP31/14, AGIP31/16, AGIP31/18, AGIP31/22, AGIP35/02, C12Q1/68, PC (C12N15/09, C12R1:93), C12N15/00, C12R1533/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S81872811 14 bp DNA linear PRI 07-APR-1999 Gogo-DRB8=WHC-DRB pseudogene [Gorilla gorilla-western lowland gorilla, ssp. gorilla, Genomic, 14 nt, segment 11 of 12].
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                                       A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
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Gorilla gorilla Gorilla
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13, A61K39/13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae, Gorilla.
1 (bases 1 to 14)
Klein,D., Vincek,V., Kasahara,M., Schonbach,C., O'hUigin,C. and
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                                                                                                                                                                                                                                                                                               Score 9.8; DB 1; Length 14;
Pred. No. 89;
0; Mismatches 2; Indels
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    14
    ^ozganism="synthetic construct"
|mol_type="genomic RNA"
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Sequence 50 from Patent WO9632483.
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/codon_start=1
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Beet Local Similarity 84.00,
Conservative
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Matches 11; Conserv
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A57558/c
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Location/Qualifiers
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Homo sapiens
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CQ836081/c
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Sukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Wang, C.-G. and Hepburn, A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 331 19-JAN-1999;
Location/Qualifiers
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Sequence 766 from Patent WO2004059001.
CQ835708.1 GI:50835242
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Sequence 331 from patent US 5861244.
AR030142.
AR030142.1 GI:5943356
                                                                                                     Masucci, M.G.
IMMUNE-EVADING PROTEINS
PATENT: WO 9632481A 50 17-OCT-1996;
MASUCCI MARIA GRAZIA (SE)
Other publication AU 5284296 961030.
Location/Qualifiers
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   A57558
A57558.1 GI:3713392
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Method for determining markers of human facial skin
Patent: WO 2004059501-A 1004 15-UUJ-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Sequence 1004 from Patent WO2004059001.
CQ835946.1 GI:50835480
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Score 9.4; DB Pred. No. 88; 0; Mismatches

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PAT 23-FEB-2005

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                              Molecular markers for the selection of soybean plants having superior agronomic performance. Performance Performance Performance Performance of 10-FB Pioneer Hi-Bred International Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holtkoetter, O., Petersohn, D., Schlotmann, K., Giesen, M. and Kesaler-Becker, D. M. dethod for determining hair cycle markers Patent: WO 2002086/1-A 257 31-MAR-2005; Henkel Kommanditgesellschaft auf Aktien (DE)
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Pred. No. 88;
0; Mismatches 1; Indels
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                                              Sequence 814 from Patent WO2005012576.
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Sequence 333 from Patent WO2005028671.
CS055436
CS058436.1 GI:62551619
                                                                                                                                          synthetic construct
synthetic construct
other sequences, artificial sequences.
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Best Local Similarity 90.9%;
Matches 10; Conservative 0
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Homo sapiens
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Best Local Similarity 90.9
Matches 10; Conservative
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                RESULT 153
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Method for determining markers of human facial skin Patent: WO 2004059001-A 1158 15-JUL-2004;
Henkel Kommanditeesellachaft auf Aktien (DB)
Location/Qualifiers
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Sequence 2625 from Patent WO2004059001.
CQ837567
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Sequence 1158 from Patent WO2004059001.
CQ836100 GI:50835634
 Pred. No. 88;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mamanlia, Butheria, Buarchontoglires, Primates, Catarrhini;
Hominidae, Homo.
                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Method for determining hair cycle markers
Patent: Wo. 2005c28671-A 348 31-MAR-2005;
Henkel Kommandicesellschaft auf Aktien (DE)
Location/Qualifiers
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Pred. No. 88;
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CS058451
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels
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Kessler-Becker, D.
Method for determining hair cycle markers
Patent: WO 2005028671-A 430 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 2907 from Patent WO02053774.
AX625866
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/db_xref="taxon:9606"

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                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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             Score 9.4; DB 1; Length 11; Pred. No. 88; 0; Mismatches 1; Indels
                                                                                                                                                         linear
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Pred. No. 88;
0; Mismatches 1; Indels
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Pred. No. 88;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                               Petersohn, D., Conradt, M. and Hofmann, K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5193 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petersohn, D., Conradt, M. and Hofmann, K. Method for determining homeostasis of the skin Patent: WO 02053774-A 7162 11-JUL-2002; Henkel Kommanditgeellschaft auf Aktien (DE)
                                                                                                                                                 Sequence 5193 from Patent W002053774.
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Sequence 7162 from Patent WO02053774.

    .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .11
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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90.9%;
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Query Match
Best Local Similarity 90.>
Best Local Similarity 90.>
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AX628152
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other sequences; artificial sequences.

E 1 (bases 1 to 12)

E 2 (bases 1 to 12)

E 3 (bases 1 to 12)

E 4 (bases 1 to 12)

E 5 (b.K.*, ii.Y.* and Gillies,S.D.

E 6 (b.K.*)

E 7 (1002523036-A 29 30-UUL-2002;

E 7 (1002523036-A/29)

E 8 (1002523036-A/29)

E 8 (1002523036-A/29)

E 8 (1002523036-A/29)

E 9 (1002523036-A/29)

E 1002523036-A/29

E 1002523036

BD240909 17-JUL-2003 Expression and export of angiogenesis inhibitors as immunofusins.
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C12N5/00,A61K37/02
Bestription of Artificial Sequence:BamHI/HindIII CC
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Patent: WO 2004005547-A 133 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
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Location/Qualifiers

    .12
        forganism="synthetic construct"
mol_type="genomic DNA"
        /db_xref="taxon:32630"

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Sequence 133 from Patent WO2004005547.
CQ766172
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Matches 10; Conservative
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AX097978
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AR475028
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence : Xbal linker
for linkage to thrA and a ttenuater"
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Method for producing l-amino acid by fermentation
Patent: WO 2005049808-A 8 02-JUN-2005;
Ajinomoto Co., Inc. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                             Patent: WO 2004005547-A 243 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)

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/organism="synthetic construct"

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                                                                                   CQ766282 12 bp DNA Sequence 243 from Patent WO2004005547. CQ766282
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Sequence 8 from Patent WO2005049808.
CS104143.1 GI:67512417
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Sequence 8 from Patent WO2005049808.
CS104143
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/note="HS motif"
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                                                                                                                                                            synthetic construct
synthetic construct
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11 CAGATGTCCTG 1
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Matches 10; Conserv
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Neri,B.P., Hall,J.G., Lyamichev,V. and Smith,L.M.
Systems and methods for invasive cleavage reaction on dendrimers
Patent: US 692917-A 415 17-FEB-2004;
Third Wave Technologies, INC; Madison, WI
Location/Qualifiers
                                                                                                                                                                                                          1. .12
/organism="synthetic construct"
/organism="synthetic construct"
/mol_type="unassigned DNA"
/dD_xrref="taxon:32630"
/hote="Description of Artificial Sequence : Xbal linker
for linkage to thrA and a ttenuater"
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Pred. No. 93;
0; Mismatches 1; Indels
                                                                                      Hashiguchi, K., Nakai, Y. and Itou, H.
Method for producing 1-amino acid by fermentation
Patent: WO 2005049808-A B 02-JUN-2005;
Ajinomoto Co., Inc. (JP)
Location/Qualifiers
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Smooth muscle cell promoter and uses thereof
Patent: WO 0118048-A 46 15-MAR-2001;
Introgene B.V. (NL)
Location/Qualifiers
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synthetic construct
synthetic construct
other sequences; artificial sequences.
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Sequence 415 from patent US 6692917.
AR475028
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Sequence 46 from Patent WO0118048.
AX097978
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W Unknown.
Unclassified.

1 (bases 1 to 13)

2 (cok, P. Dan. and Kawasaki, A.Mamoru.

2 '-modified oligonucleotides

AL Patent: US 585921.-A 26 12-JAN-1999;

Location/Qualifiers
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Sequence 39 from patent US 5783431.
AR019451
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Seguence 26 from patent US 5859221.
AR029150
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Sequence 26 from patent US 5872232.
AR036534 1 GI:5953202
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/mol_type="unassigned DNA'
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Unclassified.
1 (bases 1 to 13)
Cook, P.Dan. and Kawasaki, A. Mamoru.
2'-O-modified oligonucleotides
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/organism="unknown"
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Best Local Similarity 90.5
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
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 12 AAACGGCCTGG 2
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AR019451
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/mol_type="unassigned DNA"
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/note="variant intron-exon splice recognition sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="variant intron-exon splice recognition sequences"
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dickson, B., Berger, J., Suzuki, T. and Knoblich, J.
Method for identifying therapeutic targets by use of genetic screens in drosophila melanogaster
Patent: WO 30342407-A 2 22-MAY-2003;
BOEHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)
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                                                             Score 9.4; DB 1; Length 12; Pred. No. 93; 0; Mismatches 1; Indels
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Patent: BP 1082331-A 46 14-MAR-2001;
Introgene B.V. (NL)
Location/Qualifiers

    12
/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"

    12. 12.
    Organism="synthetic construct" /mol type="unassigned DNA" /db_xref="taxon:32630"

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Sequence 46 from Patent BP1083231.
AX138554
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Sequence 2 from Patent WO03042407.
AX772212
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90.9%;
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Matches 10; Conserv
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Peterson, T.C., Foster, L.M. and Brian, P.
Methods for generating and screening novel metabolic pathways
Patent: US 7894311-A 39 21-JUL-1998;
Location/Qualifiers
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TITLE
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Unclassified.
1 (bases 1 to 13)
Peterson, T.C. and Brian, P.
Methods for generating and screening novel metabolic pathways
Patent: Us 6242211-A 30 05-JUN-2001;
Location/Qualifiers
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Cook, P. Dan. and Kawasaki, A. Mamoru.
2'-modified oligomoralectides
Patent: US 6005087-A 26 21-DEC-1999;
Location/Qualifiers
JOURNAL Patent: US 5872232-A 26 16-FEB-1999;
ATURES Location/Qualifiers
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Sequence 26 from patent US 6005087.
AR096067
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Sequence 30 from patent US 6242211.
ARIS6401.1 GI:15125105
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Best Local Similarity 90.9
Matches 10; Conservative
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12 AAACGCCTGG 2
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12 AAACGGCCTGG 2
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Rattus norvegicus
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                    1 (bases 1 to 13)
Cook, P.Dan. and Kawssaki, A.M.
Sugar modified oligonuclectides that detect and modulate gene expression
Patent: US 6307040-A 6 23-OCT-2001;
Location/Qualifiers
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Regulatory elements in the 5' region of the vrl gene
Patent: WO 2004053120-A 270 24-JUN-2004;
Gruenenthal GmbH (DE)
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/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db xref="taxon:10116"
/noEe="V$GATA1 04"
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Sequence 26 from patent US 6399754.
AR212300. GI:21515837
13 bp
Sequence 6 from patent US 6307040.
AR174824
AR174824.1 GI:17915144
                                                                                                                                                                                                                                                                                                                               /mol_type="unassigned DNA"
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(Dassa to 13)
Cook, P. Dasa
Sugar modified oligonucleotides
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/organism="unknown"
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AR658253/C
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AX813993
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Unclassified.

S leigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Marulic-Adamac,J., Sweedler,D. and Zinnen,S.
Oligoribonucleotides with enzymatic activity
Datent: US 6617438-A 141 09-SBP-2003;
Sirna Therapeutics, Inc.; Boulder, CO
Location/Qualifiers
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Sequence 141 from patent US 6528640.
AR285769
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Sequence 141 from patent US 6617438.
AR397760. GI:40135004
Patent: US 6399754-A 26 04-JUN-2002;
Location/Qualifiers
                                                                                                                                            12.2%; Score 9.4; DE ilarity 90.9%; Pred. No. 98; Conservative 0; Mismatches

    .13
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    /mol_type="unassigned DNA"

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Best Local Similarity 90.9
Matches 10; Conservative
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     linear
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Worknown.

Unclassified.

B 1 (bases 1 to 13)

AS Cox.D.R., Margus,B.A. and Patil,N.
Genetic analysis systems and methods

AL Patent: US 6897025-A 8 24-MAY-2005;
Perlegen Sciences, Inc.; Mountain View, CA

Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other sequences; artificial sequences.
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hlarity 90.9%; Pred. No. 98;
Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for producing DNA
Patent: EP 1316605-A 5 04-JUN-2003;
NISSHINBO INDUSTRIES, INC. (JP)
Location/Qualifiers
13 bp
Sequence 8 from patent US 6897025.
AR658253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX813993 13 bp Sequence 5 from Patent BP1316605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: April 19, 2006, 16:06:39 Job time : 0.001 secs
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                                                      AR658253.1 GI:67592186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic construct
synthetic construct
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12 TAAAGAGTCAG 2
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Best Local Similarity
Matches 10; Conserv
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                                                                                        Unknown.
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Wed Apr 19 16:15:54 2006

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- nucleic search, using sw model OM nucleic April 19, 2006, 16:04:57 ; Search time 0.001 Seconds Run on:

(without alignments) 12.936 Million cell updates/sec

US-10-643-038-17\_994-1070

1 caaacaagacggcctgggga......gaagctgatgtcctgtcaag Perfect score: Sequence:

77

IDENTITY\_NUC Gapop 10.0 , Gapext 0.5 Scoring table:

`

8 segs, 84 residues Searched:

16 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 8 summaries

estdb:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	ACCESSION: AJ651054	ACCESSION: AJ590125	ACCESSION: CL983148	ACCESSION: BQ111753	ACCESSION: BQ789997	ACCESSION: CL659790	ACCESSION: CL686823	ACCESSION: CT007455
* Query Match Length DB ID	AJ651054	AJ590125	CL983148	BQ111753	BQ789997	CL659790	CL686823	T7115122
DB	П	-	-	-	-	Н	Н	Н
* Query Match Length DB	11	11	11	11	10	10	10	21
Query Match	11.7	10.9	10.9	10.1	9.6	9.6	9.6	9.6
Score	6	8.4	8.4	7.8	7.4	7.4	7.4	7.4
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Result No.	υ	υ	υ				O	

## ALIGNMENTS

7T 1 1054/c 3 AJ651054 11 bp mRNA linear EST 07-JUL-2004 17TION AJ651054 CSEORAN19 Sus scrofa cDNA clone C0003277 B19, mRNA		ORGANISM Sus scrofa ORGANISM Sus scrofa Butaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Buteleostomi;		Ą
RESULT 1 AJ651054/c LOCUS DEPINITION	ACCESSION VERSION KRYWORDS	SOURCE	REFERENCE AUTHORS	JOURN

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Direct Submission

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremicus, 91057 Bry cedex, FRANCE
Gaston Cremicus, 91057 Bry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-incolifobiogen.fr).
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
VO.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptiI(KS) R. Sitel: ECORI
R. Sitel: NOII 5' Seq Primer MilF Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Parm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.
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Arabidopsis thallana T-DNA flanking sequence, left border, clone
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T_DNA integration into the Arabidopais genome depends on sequences
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SAUSS) 1eft border; T.DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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|mol_type="ganomic DNA"
|dD_xref="taxon:3702"
|clone="563602"
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                                                                                                                                                                                                                                                                                                          /organism="Sus scrofs"
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/clone="CO003277_B19"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"
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EST597329 mixed potato tissues Solanum tuberosum cDNA clone STMCC84
                                                                                                                                                                                                                                                                                                                      CL983148 11 bp mRNA linear GSS 21-SEP-2004
GC0387 TIGEM gene trap library Mus musculus cDNA clone A012.B10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390116132205
Tel: +390116132205
Bmax: +390815790916
Email: cobellia@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 11)
Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,B.,
Barbarisi,M., Sardiello,M., Di Giorgio,F.P., Iovino,N., Zollo,M.,
Tagging genes with casestte-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
                                                                                                                                                           Gaps
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Pred. No. 1.7;
0; Mismatches 1; Indels
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                                                                                                                                                         1; Indels
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(cell_line="EM14"
(cellone lib="TiGEM gene trap library"
/note="Vector: pFLIP1"

    .11
/note="T-DNA flanking sequence
left border"

                                                                                                                   Score 8.4; DB Pred. No. 1.7; 0; Mismatches
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/organism="Mus musculus"
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/clone="A012.B10"
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/strain="129 ola"
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CL983148.1 GI:52420779
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                                                                                                  Query Match
Best Local Similarity 90.0
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11 GAGGTAAAA 2
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/clone lib="mixed potato tissues"
/note="Vector: pBluescript SK(-); Site_1: BcoRI; Site_2:
XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
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Asiegbu, F.O., Nahalkova, J. and Dean, R.A.
Selected Expressed sequence tags of CDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ789997 Heterobasidion annosum - Scots pine infection stage (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion annosum mixed EST library cDNA clone hage005aD02, mRNA sequence.
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mRNA"
/cultivar="Kennebec or Binjte"
/db xref="texon:4113"
/clone="STMCC84"
/tissue type="mixed tissues"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Solanum tuberosum"
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Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
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                                    BQ111753.1 GI:20163715
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5' end, mRNA sequence.
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CL686823 10 bp DNA linear GSS 09-JUL-2004 PRI0145b A03_2 - PRI0145b.BR (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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Mammalia, Butheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
1 (bases 1 to 10)
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Submitted (10-JUN-2005) of Genome Analysis, German Research Centre
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2 (bases 1 to 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Posmid vector"
                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida, Neodiplogasteridae, Pristionchus.

1 (bases 1 to 10)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. Appabs; an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Sommer RJ

Bvolutionary Biology

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39. Tuebingen D-72076, Germany
Tel: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
Sequenced at Vancouver, Canada.
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Equus caballus GSS, BAC clone CH241-115122, T7 end sequence,
genomic survey sequence.
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GSS; genomic survey sequence.
Equus caballus (horse)
Equus caballus
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Pristionchus pacificus
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                                                              RESULT 7
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                                                                                                                                      /mol type="mmy"
/mol type="mmy"
/db_xref="taxon:169015"
/db_xref="taxon:169015"
/db_xref="taxon:169015"
/db_xref="taxon:169015"
/dbox stage="seedling roots of scots pine were infected for 6 days with H. annosum"
/dow stage="lamb" | lbox stage | lamb | lbox stage | lbo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CL659790 10 bp DNA linear GSS 09-JUL-2004 PRI0135b B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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                                                                                       'organism="Pinus sylvestris/Heterobasidion annosum mixed
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/mol_type="genomic DNA"
/strain="California"
/db.xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus /clone lifornia"
/note="Vector: pSpifos-5 Fosmid vector"
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Pristionchus pacificus
Pristionchus pacificus
Bukaryota, Metazoa; Nematoda, Chromadorea; Diplogasterida;
Meodiplogasteridae, Pristionchus.
Srimivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Mucleic Acids Res. 32 (1), D421-D422 (2004)
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Max-Danck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.someretuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Ged primer: T7
Class: fosmid ends
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88.9%; Pred. No. 3.8;
ive 0; Mismatches 1; Indels
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ve 0; Mismatches
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Seq primer: T7 primer.
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8; Conservative
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Best Local
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COMMENT
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9.6%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 1; Indels
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2 ATACGACTC 10
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             This oligonucleotide can hybridise to nucleic acids encoding phospholipase A2 typical of the synovial fluid of patients with rheumatoid arthritis. (SF-FLA2 is more closely related to group II PLA2 enzymes such as those in rattlesnake venom than to pancreatic PLA2). The oligonucleotide (especially its phosphorothioate analogue) would be useful in inhibiting SF-PLA2 expression. SF-PLA2 secretion has been detected from a human epidermal carcinoma cell line and primary human epidermal keratinocytes. This suggests that the inhibitory oligonucleotide would be useful in the treatment of inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ61917-55 are oligonucleotides which contain a G4 stretch and which may be used for inhibiting phospholipase A2 enzyme estivity. Oligonucleotides such as these may also be used for inhibiting activity of HSV, HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * modified oligo-nucleotide contg guanine quartet - inhibits activity
viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition; replication; herpes simplex virus; HSV; HIV; aging; human cytomegalovirus; influenza virus; influenza virus; influenza virus; influenza neurological disorders; phospholipase Az activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; retard; se.
                                                                                                                                                                                                                                                               Gaps
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/note= "Phosphorothioate intersugar linkages"
                                                                                                                                                                                                                            27.3%; Score 21; DB 1; Length 21; 100.0%; Pred. No. 4.9; tive 0; Mismatches 0; Indels
                                                                                                                                                                                               Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                disorders of the skin. See AAQ14859-Q14895
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(first entry)
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                                                                                                                                                                                                                                                              21; Conservative
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Best Local Similarity
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04-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                             Phospholipase A2 group IIA; synovial; antisense modulation; inflammation; phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory; antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer; psoriasis; diabetes; ss.
disease and snake bite. They may also be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                             Gaps
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/note= "2'-0-methoxyethyl (2'-MOE)
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                                                                 Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
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                                                                                           Match 27.3%; Score 21; DB Local Similarity 100.0%; Pred. No. 4.9 es 21; Conservative 0; Mismatches
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/mod base= OTHER
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                                                           AAQ24028
ABH71039
ABH71039
ABH67527
ABH26778
ABH91036
ABH91034
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ABH77414
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Human growth hormone; granulocyte-colony stimulating factor; G-CSF; phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy; erythroid cells; beta-globin; pEC3; ss.
                                                                                                                                                                        91GB-00026984.
                                                                                                                                                                       19-DEC-1991;
                                                                                                                                                    15-JUL-1992.
                                                                                                                                  GB2251622-A
                                                                                                                Synthetic.
#XBX#X8X##XBX#XBX#
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Oligo-nucleotide analogues which modulate arachidonic acid metabolism for treatment and diagnosis of conditions caused by lipoxygenase, phospholipase, leukotriene(s) etc.

WPI; 1991-353508/48.

Claim 18; Page 54; 87pp; English

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                                                                                                                                                                                                                  in the isolation of a 200p frames containing the phospholipase A2 (PLA2) promoter sequence. This promoter sequence was used to replace the human beta-globin promoter which had been used to express the human growth hormone (HGH) gene in expression vector pBC3. The vector further comprised a promoter and a dominant control region. This vector was used in an expression system comprising a mammalian cell transformed with the vector. This expression system could be used to prepare pharmacologically useful polypeptides eg. HGH, granulocyte-colony stimulating factor (G-CSF) and PLA2, and for gene therapy. The mammalian host comprises erythroid cells and a heterologous promoter
                                                                                                                                 Expression vectors for use in mammalian cells - contain dominant control region derived from beta-globin gene.
                                                                                                                                                                                                      primer sequences given in AAQ26373-4 are PCR primers which were used
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arachidonic acid; antisense oligonucleotide; rheumatoid arthritis; osteoarthritis; lupus; anaphylaxis; urticaria; asthma; psoriasis; hepatitis; cerebral oedema; contact dermatitis; ulcerative colitis; phosphorothioate linkage; SF-PLA2; ss.
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                                                                        Antoniou M;
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                                                                      Grosveld FG,
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Pred. No. 0.59;
0; Mismatches
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                                                                                                                                                                          Disclosure, Page 32; 77pp; English.
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Best Local Similarity 90.9%;
Matches 30; Conservative
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ID AAQ14886 standard; DNA; 21
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                                                                      Hollis M, Needham MRC,
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             21-DEC-1990;
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## GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

sw model nucleic search, using OM nucleic

April 19, 2006, 16:12:08; Search time 0.001 Seconds (without alignments) 677.446 Million cell updates/sec Run on:

US-10-643-038-17\_994-1070 score: Title: Perfect #

.....gaagctgatgtcctgtcaag 1 caaacaagacggcctgggga.... Sequence:

77

IDBNTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

292 seqs, 4399 residues

Searched:

seq length: 0 seq length: 200000000 Post-processing: 88 Minimum I Maximum I

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. N-General Minimum Match 0% Maximum Match 100% Listing first 299 summaries ngsdb:\*

Chimeric phosphoro
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Human mRCKZ siRNA
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:

April 19, 2006, 16:10:20 ; Search time 0.001 Seconds (without alignments) 225.302 Million cell updates/sec

US-10-643-038-17\_994-1070 77 1 caaacaagacggcctgggga......gaagctgatgtcctgtcaag 77 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 0.5 Scoring table:

100 segs, 1463 residues Searched:

Issued, Patents-NA Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

isadb:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	# E			SUMMAKIES		
Score	Match	Match Length	DB	TD CI	Description	Ę
28.2	36.6	33	-	US-08-186-895-4	Sequence	4, Appli
21	27.3	21	-	US-07-847-055A-13	Sequence	13, Appl
21	27.3	21	-	US-08-403-888A-59	Sequence	
16	20.8	20	-	PCT-US96-09009-9		
4.8	19.2	21	-	US-09-581-831-3	Sequence	3, Appli
4.4	18.7	17	-	US-09-866-108A-10026	Sequence	10026, A
4.4	18.7	17	Н	US-09-866-108A-10027	Sequence	10027, A
4.4	18.7	18	Н	US-09-205-860-40		40, Appl
14	18.2	17	П	US-09-866-108A-10024		10024, A
14	18.2	17	-	US-09-866-108A-10025	Sequence	10025, A
4.	17.4	17	-	US-09-866-108A-10028	Seguence	10028, A
7	17.1	18	-	US-08-096-947-14	Sequence	14, Appl
3.5	17.1	18	-	US-08-096-947-17	Sequence	17, Appl
3.2	17.1	18	-	US-07-919-140B-14	Sequence	14, Appl
3.2	17.1	18	٦	US-07-919-140B-17	Sequence	17, Appl
3.5	17.1	18	-	US-08-916-232-14	Sequence	14, Appl
3.2	17.1	18	-	US-08-916-232-17	Sequence	17, Appl
3.2	17.1	18	-	US-09-657-986B-6	Seguence	6, Appli
3.2	17.1	18	Н	PCT-US93-06939-14		14, Appl
3.2	17.1	18	н	PCT-US93-06939-17		_
13	16.9	17	-1	US-09-866-108A-10023		10023, A
12.4	16.1	17	Н	US-09-474-432B-817		817, App
2.4	16.1	17	-	US-09-476-387-816		
12.4	16.1	17	Н	US-09-866-108A-10029		
12	15.6	-	ч	US-09-866-108A-10022		10022, A
80	15.3	16	~	US-09-371-772B-6986		6986, Ap
11.8	15.3	16	-	5168062-12		5168062
11.8	15.3	16	-	5168062-13	Patent No.	5168062
11.4	14.8	-	~	US-08-173-489C-4	Seguence	4, Appli
11.2	14.5	16	-	US-08-308-892A-12		
11.2	14.5	16	-	US-09-060-299-450		450, App
7.5	14.5	16	-	US-09-402-923A-450		450, App
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ALIGNMENTS

RESULT 1

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REFERENCE/DOCKGT NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
NATI-SENSE: yes
US-07-847-055A-13
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/07847055A

Patent No. 5530114

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Arachidonic Acid Metabolism
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Moodcock Washburn
ADDRESSEE: Kurtz Mackiewicz & No. 5530114ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2003-5601

ZIP: 2003-5601

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,895
FILING DATE: 27-JAN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/046,383
FILING DATE: 09-ARR-1993
APPLICATION NUMBER: US/08/046,383
FILING DATE: O9-ARR-1993
APPLICATION NUMBER: US/08/046,383
FILING DATE: O1-ARR-1993
APPLICATION NUMBER: US/08/04/14
ATTORNEY/AGENT INPORMATION:
TELEPHONE: CO2-861-3000
TELEPHONE: 202-861-3000
TELEPRANCTON TON NUMBER: PNK/3893/93802/MJW
TELECOMMUNICATION NUMBER: PNK/3893/93802/MJW
TELEFAX: 6714627 CUSH
TELEFAX: 6714627 CUSH
TELEFAX: 31 base pairs
TELENGTH: 33 base pairs
TWDENATION POR REQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
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              Sequence 4, Application US/08186895
| Patent No. 5538885
| GENERAL INFORMATION:
| APPLICANT: Hollis, Melvyn
| APPLICANT: Gooding, Clare
| APPLICANT: Gooding, Clare
| TITLE OF INVENTION: Expression Systems
| OVARESPONDENCE ADDRESS: 10
| CORRESPONDENCE ADDRESS: 3
| ADDRESSEE: CLSHWAN, Darby & CUSHWAN
| STREET: 1615 L Street, N.W.
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Best Local Similarity 90.9%
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STRANDEDNESS: single
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US-08-186-895-4
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-07-847-055A-13/c
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Gaps
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COMPUTER KEALALE FORM:

MEDIUM TYPE: DISKETTE,

COMPUTER: IBM PS/2

COMPUTER: IBM PS/2

COMPUTER: IBM PS/2

SOFTWARE: WORDERFECT 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/847,055A

FILING DATE: 19920403

CLASSIPICATION DATA:

APPLICATION NUMBER: US/07/516,969

FILING DATE: APPLICATION:

APPLICATION NUMBER: US/07/516,969

FILING DATE: APPLICATION:

ANDRE: JOHN W. Caldwall

REGISTRATION NUMBER: 28,937

REFERENCE/DOCKET NUMBER: 151S-182

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

MENGTH: 21
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CUMPUTRY: PA

COMPUTRY: 19103.

COMPUTRY: READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,888A
FILING DATE: 12-UNN-1995
CLASSIFTCATION: 435
PRIOR APPLICATION NUMBER: 07/954,185
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORWATION:
NAME: PAUL K. LEGARAT
REFERENCE/DOCKET NUMBER: 38,534
REFERENCE/DOCKET NUMBER: 1515-1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 ATACAACTCTGGAGTCCTCTG 40
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Sequence 3, Application US/09581831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GV. Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: RANKE, David K.
APPLICANT: RANK, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
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                                                                                                                                                                                 Gaps
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APPLICANT: Siracutes, Linda D.
APPLICANT: Siracutes, Linda D.
APPLICANT: Chepenik, Kenneth P.
TITLE OF INVENTION: RISK FACTOR FOR COLORECTAL CANCER
TITLE OF INVENTION: AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF DETECTING THE SAME
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSER: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
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                                                                                                                                      Score 21; DB 1; Length 21;
Pred. No. 0.94;
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                                                                                                                                                                                 0; Indels
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                                                                                                                                      Query Match 27.3%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 0.5 Matches 21; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Liberty Place, 46th Ploor CITY: Philadelphia STATE: Pennsylvania COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09009
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/484,359
APLICATION NUMBER: US 08/484,359
FILING DATE: 07-JUN-1995
CLASSIFICATION:
NAME: PLACON NUMBER: 33,229
REPERRICE/DOCKET NUMBER: 33,229
TELECONOUNICATION INPORMATION:
TELECONOUNICATION INPORMATION:
TELECONOUNICATION INPORMATION:
TELECONOUNICATION INPORMATION:
TELECONOUNICATION 118-05-3439
TELERERX: 215-568-3439
                                                                                                                                                                                                                                                                                                                 20 ATACAACTCTGGAGTCCTCTG 40
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100.08; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGATGTCCTGTCAAG 77
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SEQUENCE CHARACTERISTICS:
LENGTH: 21
                                     TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 16; Conserva
                                                                              ; TOPOLOGY: linear
US-08-403-888A-59
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PCT-US96-09009-9
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RESULT

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APPLICANT: ZAPHIROPOULOS, PETER G.
APPLICANT: ZAPHIROPOULOS, PETER G.
APPLICANT: KOGREMAN, PRIIT
APPLICANT: KOGREMAN, PRIIT
APPLICANT: GARINAN
TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE HUMAN SUPPRESSOR OF FUSED
TITLE OF INVENTION: GENE
TITLE OF INVENTION: GENE
TITLE OF INVENTION: GENE
TITLE OF PLICATION NUMBER: DS 099-6058
CURRENT FILING DATE: 2000-08-21
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-19
PRIOR PLICATION NUMBER: 9704788-0
PRIOR PLICATION NUMBER: 9704788-0
PRIOR PLICATION NUMBER: 997-12-19
PRIOR PLICATION NUMBER: 9802293-2
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 21
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APPLICANT: HANZEL, DAVIG K.
APPLICANT: RANK, DAVIG K.
APPLICANT: RANK, DAVIG R.
APPLICANT: SHANNON, MARCH
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEGONICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-00-27
PRIOR PILING DATE: 2001-01-30
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US-09-581-831-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10026, Application US/09866108A Patent No. 6686188
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RESULT 8
US-09-205-860-40/c
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APPLICANT: SEALENS
APPLICANT: BANK, Sharron G.
APPLICANT: BANK, David K.
APPLICANT: BANK, David K.
APPLICANT: BANK, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: SHANKON, MAK
TITLE OF INVENTION: WACSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE CURRENT FILING DATE: 2001-05-26
PRIOR PELICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-04
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PILING DATE: 2001-01-30
PRIOR PIL
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PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10026
LENGTH: 17
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18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels
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Pred. No. 11;
0; Mismatches
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93.8%;
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                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108A-10026
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US-09-866-108A-10027
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Best Local Similarity
Matches 15; Conserv
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US-09-866-108A-10027
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Sequence 10.0 Application US/09205860

PARTICANT: Lear N. Cowner:
APPLICANT: Lear N. Comner:
APPLICANT: Lear N. Cowner:
APPLICANT
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: WOOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: ADDITION: WINDSLANDING GRADE DEFENDS DE IN NOTATION PRINCE OUR RENT APPLICATION NUMBER: US/09/866,108A
CURRENT APPLICATION NUMBER: US 60/207,456
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-10-26
FRIOR PILING DATE: 2000-10-27
FRIOR APPLICATION NUMBER: US 60/236,359
FRIOR PILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: PCT/US01/00666
FRIOR PILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
                                                                                                                                                                           Gaps
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                                                                                                    Score 14; DB 1; Length 17; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 17;
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                       ;
                                                                                                                                                                           Mismatches
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Patent No. 6686188
SEQ ID NO 10025
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10025, Application US/09866108A Patent No. 6686188 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 18.2%; Soc
Best Local Similarity 100.0%; P;
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.2%; Sc
llarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                        27 TCTGGAGTCCTCTG 40
                                                                                                                                                                                                                                                                                                            4 rerecastrerere 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 rerecasereere 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-09-866-108A-10025
; ORGANISM: Homo sapiens
US-09-866-108A-10024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-866-108A-10025
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APPLICANT: BANN, Sharron G.
APPLICANT: BANN, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wencheng
APPLICANT: SHANNON, MAKE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEGONICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PLILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLILING DATE: 2001-01-30
PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WordPerfect 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purified Thermostable
Pyrococcus Puriosus DNA
Ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08096947
Fatent No. 5506137
GENERAL INFORMATION:
APPLICANT: Bric J. Mathur
APPLICANT: Bdward J. Marsh
ITILE OF INVENTION: Purified Thermory
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSED: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Prancisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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TELEX: 278356
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 bases
                                                                                                                                                                                              HYPOTHETICAL: n
HYPOTHETICAL: no
HATI-SENSE: no
US-08-096-947-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: no
US-07-919-140B-14
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       APPLICATION UNBER: US/08/096,947
FILING DATE: 19930722
GLASSIFCATION: 435
FILING DATE: 19930722
FILING DATE: 10930722
FILING DATE: 07/919,140
FILING DATE: 01/y 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
FREGISTRATION NUMBER: STRG 20081 USA
TELECOMMUNICATION INFORMATION:
TYPE: MULCULE TYPE: chemically Synthesized Oligomucleotide
TOPOLOGY: linear
MULCULE TYPE: Chemically Synthesized Oligomucleotide
HYPOTHETICAL: NO
ANTI-SENDE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08096947
Patent No. 5506137
GENERAL INFORMATION:
APPLICANT: Eric J. Mathur
APPLICANT: Beward J. Marsh
TITLE OF INVENTION: Purified Thermostable
TITLE OF INVENTION: Purified Thermostable
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Perry Building
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOMETREE IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,947
FILLING DATE: 19930722
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/919,140
FILLING DATE: UJLY 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: ALBERTE P. Halluin
REGISTRATION NUMBER: 5,227
REFERENCE/DOCKET NUMBER: STRG 20081 USA
TELECHONE: (415) 433-4150
TELEPHONE: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GGATACAACTCTGGAGTC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GGACACAACCTTGGAGTC 1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-096-947-17
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                                                                                                                                                                                                                                   ACESULT 14
US-07-919-140B-14/C

; Sequence 14, Application US/07919140B
; Patent No. 5700672
; GENERAL INFORMATION:
; APPLICANT: Edward J. Marhur
; APPLICANT: Edward J. Markin
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF EQUANCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
CONNTEY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.2; DB 1; Length 18; Pred. No. 18; 0; Mismatches 3; Indels
                                                                                                                                DB 1; Length 18;
                                                                                                                                                                        Indels
TOPOLOGY: linear MOLECULE TYPE: Chemically Synthesized Oligonucleotide HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Chemically Synthesized Oligonucleotide
                                                                                                                              Score 13.2; DE Pred. No. 18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM;
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPACE
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/919,140B
FILING DATE: Ully 23, 1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
RESISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 21,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELESTAX: 415-854-3694
TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  18 GGATACAACTCTGGAGTC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GGATACAACTCTGGAGTC 35
                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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California
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-916-232-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-916-232-14/C

Sequence 14, Application US/08916232

Sequence 14, Application US/08916232

Patent No. 6280998

GENERAL INFORMATION:
APPLICANT: Eric J. Mathur
APPLICANT: Warren B. Schoettlin
TITLE OF INVENTION: Purified Thermostable Pyrococcus
TITLE OF INVENTION: Purified Thermostable Pyrococcus
TITLE OF INVENTION: Purified Thermostable SCORRESPONDENCES: 17

CORRESPONDENCES: 17

STREET: 2730 Sand Hill Road
                                                                                                                                                             US-07-919-140B-17

Sequence 17, Application US/07919140B

Sequence 17, Application US/07919140B

Patent No. 5700672

GENERAL INFORMATION:

APPLICANT: Eric J. Mathur

APPLICANT: Edward J. Marsh

APPLICANT: Bdward J. Marsh

TITLE OF INVENTION: Purified Thermostable Pyrococcus

TITLE OF INVENTION: Purified Thermostable Pyrococcus

TITLE OF SEQUENCES: 17

CORRESPONDENCE ADDRESS: 17

SORRESPONDENCE ADDRESS: 17

STREET: 2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTER: USA
ZIP: 94025
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION INVERS: US/O/919,140B
FILING DATE: July 23, 1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
RAGIGSTRATTON NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 3142-013
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GGATACAACTCTGGAGTC 35
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        18 GGACACAACCTTGGAGTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Menlo Park
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-07-919-140B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
        윱
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Tip: 3-610-35.

COMPUTER HADDALE FORM:
MEDIUM THER: 10-90-90 Disk
COMPUTER: 134 PC Compatible
COMPUTER: 134 PC COMPAGE
COMPA
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| GENERAL INFORMATION:
| APPLICANT: Madison, Edwin L.
| APPLICANT: Semple, Joseph Edward
| APPLICANT: Combs, Gary Samuel
| APPLICANT: Combs, Gary Samuel
| APPLICANT: Meiner, John Eugene
| APPLICANT: Ong, Edgar O.
| APPLICANT: Araldi, Glan Luca
| TITLE OF INVENTION: Inhibitors of Serine Protease Activity of Matriptase or
| TITLE OF INVENTION: MTSP1
| FILE REFERENCE: Corvea 555/049
| CURRENT APPLICATION NUMBER: US/09/657,986B
| CURRENT APPLICATION NUMBER: US/09/657,986B
| CURRENT PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 11
| SEQ ID NO 6
| LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: Chemically Synthesized Oligonucleotide HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of artificial sequence: CTHER INFORMATION: oligonucleoide primer US-09-657-9868-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Eric J. Mathur
APPLICANT: Edward J. Marsh
APPLICANT: Warren E. Schoettlin
TITLE OF INVENTION: Purified Thermostable
TITLE OF INVENTION: Pyrococcus Furiosus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%; Score 13.2; I 83.3%; Pred. No. 18; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.1%; Score 13.2; Dest Local Similarity 83.3%; Pred. No. 18; Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-06939-14/c; Sequence 14, Application PC/TUS9306939; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 6, Application US/09657986B; Patent No. 6797504
                NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,27
REFRENCE/DOCKET NUMBER: 8142-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-364
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GGATACAACTCTGGAGTC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGACACAACCTTGGAGTC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 GGAGTCCTCTGAGAGGTA
ATTORNEY/AGENT INFORMATION:
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Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: no
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US-09-657-986B-6/c
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Gaps
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                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
COMPUTER: Diskette, 3+ inch, 1.4 Mb storage
COMPUTER: Diskette, 3+ inch, 1.4 Mb storage
COMPUTER: DISKETTER FC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06939
FILING DATE: 19930722
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Section 17 Application PC/TUS9306939
SEMBRAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eric J. Mathur
APPLICANT: Edward J. Mathur
TITLE OF INVENTION: Purified Thermostable
TITLE OF INVENTION: Pyrococcus Furiosus DNA
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STRET: 2001 Ferry Building
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP:
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MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                     PRICIAL DATA:
PRICICATION NUMBER: 07/919,140
FILING DATE: July 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET UNBER: STRG 20081 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 GGATACAACTCTGGAGTC 35
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TELEST: 278356
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.3
Matches 15; Conservative
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CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ASONICA-7
FULE REPERENCE: ASONICA-7
CURRENT PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-27
PRIOR PILING DATE: 2000-05-7
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
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Pred. No. 18;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemically Synthesized Oligonucleotide
                                              PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/919,140
FILING DATE: July 23, 1992
ATTORNEY/AGRAT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: STRG 20081 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPAS: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 10023, Application US/09866108A Patent No. 6686188 GENERAL INFORMATION:
APPLICATION NUMBER: PCT/US93/06939
FILING DATE: 19930722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 GGATACAACTCTGGAGTC 35
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Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 278356
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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PCT-US93-06939-17
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US-09-866-108A-10023
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APPLICANT: Beaudry, Amber
APPLICANT: Beaudry, Amber
APPLICANT: Rarpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Adamic, Jasenka
APPLICANT: Zinnen, Bhawn
TITLE OF INVENTION: NUCLEOCIDE triphosphate and their incorporation into oligonucleot
FILE REFERENCE: MEHBOO-831-B (247/276)
CURRENT FILING DATE: 1999-12-19
FRIOR APPLICATION NUMBER: US 60/064,866
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-04-29
PRIOR PILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE PACENTION OF SEQ ID NOS: 1526
SEQ ID NO 817
LENGTH: 17
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APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Beaudry, Amber
APPLICANT: Rarpeisky, Alex
APPLICANT: Sweedler, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nuclectide Triphosphate and their Incorporation into Oligonucleotif
FILE REPERENCE: MBHB00-831-C (249/073)
CURRENT APPLICATION NUMBER: US/09/476,387
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                                                                                                                                                                                                                            Indels
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                                                                                                                                                                       Query Match 16.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 19; Matches 13; Conservative 0; Mismatches
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Best Local Similarity 71.4%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 817, Application US/09474432B
Patent No. 6528640
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Patent No. 6617438
GENERAL INFORMATION:
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                                                                         TYPE: DNA
CRGANISM: Homo sapiens
US-09-866-108A-10023
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US-09-474-432B-817
Patent No. 6686188
SEQ ID NO 10023
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RESULT 25
US-09-866-108A-10022
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PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: GB 24263.6

PRIOR PLICATION NUMBER: GB 24263.6

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLING DATE: 201-01-30

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PRIOR PLING DATE: 2001-01-30
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APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

PILE REPERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A
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                         PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR PLING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR PLING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/186,675
PRIOR PILING DATE: 1998-11-04
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SEQ ID NO 916
LENGTH: 17
   2001-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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US-09-476-387-816
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CORGANISM: Homo sapiens
US-09-866-108A-10029
CURRENT FILING DATE:
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US-09-866-108A-10029
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
DB 1; Length 17;
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                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Score 12.4; 1
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: AECMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-371-772B-6986/C
; Sequence 6986, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: McSwiggen, Jim
; APPLICANT: McSwiggen, Jim
                                                                                                                                                                                                                                                                                                                           Sequence 10022, Application US/09866108A Patent No. 6686188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                      29 TGGAGTCCTCTGAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 TCTGGAGTCCTC 38
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CORGANISM: Homo sapiens
US-09-866-108A-10022
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                                                                                                                                                                                                                                                      Score 11.8; DB 1; Length 16; Pred. No. 28;
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DESCRIPTION: third strand derived from c-myc
DESCRIPTION: sequence region in Seq ID No. 58612443
POTHETICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
APPLICANT: HERBURN,
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OP SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSER: PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĩ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 : FROM 1 TO
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Pred. No. 32;
0; Mismatches
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIPROCATION AND DATA:

APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIPROCATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/0/68,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:

NAME: Handelman, JOSEPH H.

REGISTRATION NUMBER: 26,179
REFERENCE/POCKET NUMBER: U9:18-6
TELECOMMUNICATION INFORMATION:

TELEFONDE: (ALLOCTICH) (212) 708-1880
TELEFONDE: (ALLOCTICH) (212) 708-1880
TELEFONDE: (ALLOCTICH) (212) 246-8959
INFORMATION FOR SEQ ID NO: 4: SEQUENCE: CONTENT OF SEQUENCE: CONTENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Sequence 4, Application US/08173489C
Patent No. 5861244
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STRANDEDNESS: single stranded
               APPLICATION NUMBER: 58,662
FILING DATE: 22-MAY-1987
APPLICATION NUMBER: 696,617
FILING DATE: 30-JAN-1985
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Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    63 TGATGTCCTGTCAAG 77
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Best Local Similarity 92.3
Matches 12; Conservative
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US-08-173-489C-4/c
                                                                                                                                                                    LENGTH: 16
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                                                                                                                                          SEQ ID NO:13
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APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: MBHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 6986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITE OF INVENTION: TRANSFER VECTORS AND MICROORGANISMS;
CONTAINING HUMAN CYTOMEGALOVIRUS IMMEDIATE-EARLY
PROWOTER-REGULATORY DAM SEQUENCE
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
PREMIT APPLICATION NATA:
PRILING DATE: 10-SEP-1990
PRILING DATE: 5-OCT-1988
FILING DATE: 5-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 16;
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APPLICANT: STINSKI, MARK F.

TITLE OF INVENTION: TRANSPER VECTORS AND MICROORGANISMS;
CONTAINING HUMAN CYTOMEGALOVIRUS IMMEDIATE-EARLY
; PROMOTER-REGULATORY DNA SEQUENCE
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION DATA:
; RILING DATE: 10-SEP-1990
; FILING APPLICATION WHERE: 256,134
; RILING DATE: 5-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.3%; Score 11.8; 86.7%; Pred. No. 28
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 13; Conserva
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;Patent No. 5168062
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TYPE: nucleic acid
STRANDEDNESS: double
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US-09-402-923A-450
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US-09-060-299-450
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                                                                            RESULT 30
US-08-308-892A-12
; Sequence 12, Application US/08308892A
; Patent No. 5500341
; GENERAL INFORMATION:
; AFPLICANT: Spears, Patricia A.
; TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM KANSASII
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Company
; ADDRESSER: Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Merriman, Tony R
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 6545137el Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,892A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Patent No. 6545137
GENERAL INFORMATION:
APPLICANT: Todd, John A
APPLICANT: Hees, John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caskey, Charles T
Cox, Roger D
Gerhold, David
Hammond, Holly
Hey, Patricia
Kawaguchi, Yoshihiko
Merriman, Tony R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILLING DAVIES:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R. 32,135
REGISTRATION NUBBER: P-315
REFERENCE/DOCKET NUMBER: P-315
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
ILRNGTH: 16 base pairs
ITYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                           STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 81.2
Matches 13, Conservative
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14 GAGAGGAAAGAG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 31
US-09-060-299-450
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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COUNTER RELABLE FORM:

WEDIUT TEE: 105 Per 105 Acres 105
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RESULT 35
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Patent No. 6685948

GENERAL INPORMATION:
APPLICANT: Markoff, Lewis
TITLE OF INVENTION: REPLICATION-DEFECTIVE DENGUE VIRUSES
TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS
TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS
TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS
TITLE OF INVENTION: THAT ARE REPLICATION NUMBER: US/09/798,542
CURRENT APPLICATION NUMBER: DS/02-05
PRIOR PELLING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: US 60/098,981
PRIOR PILING DATE: 1998-09-02
PRIOR PELLING DATE: 1998-09-02
SOFTWARE: PSECEN FOR Windows Version 4.0
SOFTWARE: PSECEN FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.5%; Score 11.2; DB 1; Length 16; Best Local Similarity 81.2%; Pred. No. 35; Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 16;
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                                 PILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY, AGRAT INFORMATION:
NAME: B.J. Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE, DOCKET NUMBER: 620-81
TELESCOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEPRAK: (703)816-4100
INFORMATION FOR SEQ ID NO: 450:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 DASE PAIRS
                       APPLICATION NUMBER: PCT/GB98/01102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 450: US-09-402-923A-450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
US-09-875-453B-65/c
; Sequence 65, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: RNA
; ORGANISM: Flavivirus, West Nile
US-09-798-542-9
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 TGAGAGGTAAAGAGCC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 rcacaderaageaecc 16
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crcrrcrcrcrarca 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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US-09-798-542-9/c
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### APPLICANT: | MAIN |
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RESULT 38
US-08-319-492B-358/C
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                                                                                                                                                                                                                    Score 11; DB 1; Length 15;
Pred. No. 35;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 36
US-08-182-968A-186/C
is Sequence 186, Application US/08182968A
j Patent No. 5610054
j GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR TITLE OF INVENTION: INHIBITING HERAITIS C
TITLE OF INVENTION: INHIBITING HERAITIS C
TITLE OF INVENTION: INHIBITING HERAITIS C
TITLE OF INVENTION: URUS REPLICATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
STREET: Suite 4700
STATE: California
                                                                                                                                                                                                                    Query Match

14.3%; Score 11; DB
Best Local Similarity 100.0%; Pred. No. 35;
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATUS:
COUNTRY: US.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 13.5" Diskette, 1.44 Mb
MEDIUM TYPE: 13.5" Diskette, 1.44 Mb
MEDIUM TYPE: 13.0 mbatible
OPERATING SYSTEM: IBM COMPATIBLE
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
PILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
RELEPHONE (213) 499-1600
TELEPHONE (213) 499-1600
TELEPRAX: (213) 955-0440
SEQUENCE CHARACTERISTICS:
               TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENESS: single
1 TOPOLLGY: linear
US-08-363-240A-116
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 CCAAGATGATGTCC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserva
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  TELEFAX:
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Sequence 357, Application US/08319492B

Patent No. 5616488

GENERAL INFORMATION:

APPLICANT: Sullivan, Sean M.
APPLICANT: Standsomb, Dan T.

TITLE OF INVENTION: RECONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF LI-5

NUMBER OF SEQUENCES: 751

CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 4700

CITY: Los Angeles
STREE: California
COUMPRY: U.S.A.

ZIP: 20071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Patent No. 5616488
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Bullivan, Kenneth G.
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 18H Compatible
COMPUTER: 18H Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: OCCODER 7, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: 408.759
FILING DATE: January 19, 1993
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INPORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10.8; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%;
85.7%;
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid

STRANDEDNESS: single

; TOPOLOGY: linear

US-08-291-932A-373
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OR CONDITIONS RELATED TO LEVELS OF IL-5
                                                                                                                                       STREET: Sulte 4,vu
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 15.5" Diskette, 1.44 Mb
MEDIUM TYPE: 15.5" Diskette, 1.44 Mb
MEDIUM TYPE: 10.5" DISKETTE, 1.44 Mb
MORTANTE NOT DATA: 10.5 No.5
MEDIUCATION NUMBER: 10.5 No.5
MEDIUCATION NUMBER: 07/989, 849
PILING DATE: DECEMBET 7, 1992
MEDIUCATION NUMBER: 07/989, 849
PILING DATE: DECEMBET 7, 1992
MEDIUCATION NUMBER: 209/276
MERSTRATION NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEBHONE: (213) 955-0440
TELERENOR: 67-3510
TELERENOR: 15 DASS PAISS
MENDET: 15 DASS PAISS
MENDET: MENDET: 15 DASS PAISS
MENDET: MENDET: 15 DASS PAISS
MENDET: MENDET: 15 DASS PAISS
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APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSaviggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: NP-KB
NUMBER OF SKUURENES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Galifonnia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10.8; I
Pred. No. 38;
0; Mismatches
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US-08-291-932A-373
US-08-291-932A-373
Sequence 373, Application US/08291932A
Patent No. 5558780
GENERAL INFORMATION:
                                               NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 ACTCTGAAGTCTTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-319-492B-358
         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071-2066
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Gaps
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Pred. No. 38;
3; Mismatches 2; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION DATA: including application
PRIOR APPLICATION DATA: including application
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardhard J.
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 208/157
TELECOMMUNICATION NUMBER: 208/160
TELERRAX: (213) 955-0440
TELERRAX: (7-3510
INFORMATION POR SEG ID NO: 373:
SEQUENCE CHARRACTERISTICS:
TENDATH: 15 Dase palrs
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TOPOLOGY: linear
              US-09-064-156A-186
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US-08-171-385-28
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                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 41
US-09-064-156A-186/C
Sequence 186, Application US/09064156A
Patent No. 6123966
GENERAL INFORMATION:
APPLICATE OF INVENTION:
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: URUS REPLICATION
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SURGENCES: 498
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                   Score 10.8;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAK: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                             57 CGAAGCTGATGTCC 70
                                                                                                                                                                                                                                                                                                                                                          15 ccaadardardrcc 2
                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
US-08-774-306A-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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                                              Gaps
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                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Berzinski, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
Score 10.8; DB 1; Length 15; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10.4; DB 1; Length 13; Pred. No. 38;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FLING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CIMDAIA, Michele A
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 1050.0410000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                              0; Mismatches
                                                                                                                                                                                                         US-08-282-197C-36
; Sequence 36, Application US/08282197C
; Patent No. 5871730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.5%;
      Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                    57 CGAAGCTGATGTCC 70
                                                                                                                             15 ccaacarcarcrcc 2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 GCGAAGCTGATG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
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0; Mismatches
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan Esq., Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/COCKET NUMBER: 181411-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENNESS: single
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      13.0%; Score 10; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CHOATE, HALL & STEWART STREET: 53 State Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 248-4000 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AGCCAGCGAA 60
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
HYPOTHETICAL:
ANTI-SENSE: N(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-430-536A-13
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US-08-430-536A-13
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Sequence 13, Application US/08351748

Patent No. 5599672

GENERAL INFORMATION:

APPLICANT: Liang, Peng
APPLICANT: Blanchi, Cesario, P.

ITILB OF INVENTION: MESSENGER RNAS

NUMBER OF SEQUENCES: 2

CORRESPONDENS:
ADDRESSE: CHOATE, HALL & STEWART

STREET: 53 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: EN PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: BAPELCATION DATA:

RELIGG DATE:

CURSENT APPLICATION DATA:

PRIOR APPLICATION DATA:

SHICK APPLICATION DATA:

HONGEST APPLICATION DATA:

PRIOR APPLICATION DATA:

HONGEST APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.0%; Score 10; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 35; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                       CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
CUNRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05433/006001
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: FRASEr, Janis K.
REGISTRATION NUMBER: 34,819
REPRENCE/POCKET NUMBER: 0543;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: (617) 542-8966
TELEX: 200154
INPORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AGCCAGCGAA 60
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US-08-171-385-28
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US-08-351-748-13
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ö ö Gapa Gapa ö ö DB 1; Length 10; 35; 13.0%; Score 10; DB 1; Length 10; ilarity 100.0%; Pred. No. 35; Conservative 0; Mismatches 0; Indels Sequence 13, Application US/08430536A
Patent No. 5655547
GENERAL INFORMATION:
APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: MESSENGER RNAS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: 0; Indels CUUNTRY: USA
ZIP: 02109-2891
COMPITER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,536A
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Herschbach Ph.D., Brenda M.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 181411-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERPHONE: (617) 248-5000

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COMPUTER READABLE FORM:
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US-08-678-280-14
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                                                                                                                                                                                                                                                                                US-08463-600

| US-08463-600
| Patent No. 575976
| Patent No. 576976
| Patent No. 5769
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US-08-678-280-14
i Sequence 14, Application US/08678280
i Patent No. 5776633
i GENERAL INFORMATION:
APPLICANT: SMITH, HELENE S.
APPLICANT: GHOW, LING-CHEN
ITTLE OF INVENTION: TRACETS FOR BREAST CANCER DIAGNOSIS AND TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 14
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
STREET: 755 Page Mill Road
CONTY: Palo Alto
STREET: California
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 494-0792
TELEX: 706141
INPORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                      51 AGCCAGCGAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-463-660-14
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WENTINE TYPE: # | Prop. disk.

GENETIES: 18 PC Compatible
OPERATINE SYSTEM: PCD-026/95-D08

GORRATHS SYSTEM: PCD-026/95-D08

GORRATHS SYSTEM: PCD-026/95-D08

GORRATH MORER: 10 | Vole (79, 20)

FILING DATE: 11 | Vole (79, 20)

ATTORNEY MORER: 40, 233

REFERENCE/DOCKET WINDER: 20889-20001.20

TELEPAX: (415) 434-0732

MANE: SCHIE (1 A. Matchael)

FELENCE CHARACTERITICS: 131-560

TELEPAX: (415) 434-0732

MORER: POS-430 | MATCHAEL | MATCHAEL
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                                                                                                                                                                                                              Gaps
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| Batent No. 5965409
| GENERAL INFORMATION:
| APPLICANT: Pardee Ph.D., Arthur B.
| APPLICANT: Liang Ph.D., Peng
| TITLE OF INVENTION: SYSTEM FOR COMPARING LEVELS OR AMOUNTS
| TITLE OF INVENTION: OF MRNAS
| NUMBER OF SEQUENCES: 27
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: ADD
                                                                                                                                                                                                         ö
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                                                                                                                        Score 10; DB 1; Length 10;
Pred. No. 35;
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                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY TO SA

ZIP: 02109-2891

COMPUTER READBLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,547
FILING DATE: 19-UL-1995
FILING DATE: 19-UL-1995
ATTORNEY/AGENT INFORMATION:
NAME: JATCATION: A35
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0181411-0013
TELEPHONE: (617) 248-5000
TELEPHONE: (617) 248-5000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08942819
Patent No. 5965707
GENERAL INFORMATION:
APPLICANT: Tam, See-Ying
APPLICANT: Tam, See-Ying
APPLICANT: Galli, Stephen
IIILE OF INVENTION: RIN2, A NOVEL INHIBITOR OF
                                                                                          13.0%; Scur
100.0%; Pre
0; /
                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                  51 AGCCAGCGAA 60
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linear
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US-08-684-547-13
; TOPOLOGY:
US-08-582-261A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-684-547-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 50
US-08-942-819-3
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## Sequence 28, Application US/08361441B
## Septicant Russell, Mary E.
## APPLICANT: Russell, Mary E.
## TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
## TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
## STATE PORTOR READARS:
## STATE: MA
## COUNTRY: USA
## COUNTRY: USA
## COUNTRY: USA
## COUNTRY READABLE FORM:
## MEDIUM TYPE: Diskette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.0%; Score 10; DB 1; Length 10;
100.0%; Pred. No. 35;
tive 0; Mismatches 0; Indels
TITLE OF INVENTION: RAS-MEDIATED SIGNALING
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEB: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,819
FILING DATE: 02-OCT-1997
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/058,520
FILING DATE: 11-SEP-1997
ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: BIH96-13pA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: PEACESQ for Windows Version 2.0b
SUPTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PAPLICATION NUMBER: 08/171,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AGCCAGCGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                               02173
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US-08-361-441B-28
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GENERAL INFORMATION:
APPLICANT: Duret, Matchias
APPLICANT: Nees, Matchias
APPLICANT: Nees, Matchias
APPLICANT: Nees, Matchias
TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
TITLE OF INVENTION: SCHU 204 (09902857)
FILE REFERENCE: SCHU 204 (09902857)
FILE REFERENCE: 1999-09-03
PRIOR APPLICATION NUMBER: PCT/DE97/02660
PRIOR APPLICATION NUMBER: DE 196-11-12
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
SEQ ID NO 3: 4
LENGTH: 10
      Gaps
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Sequence 132 Application US/09313221A

Patent No. 6468743

APPLICANT: Thomas L. Romick (Inventor)

APPLICANT: Thomas L. Romick (Inventor)

APPLICANT: Mark S. Fraser (Inventor)

TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL

TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS

FILE REFERENCE: HUNT-042704

CURRENT APPLICATION NUMBER: US/09/313,221A

CURRENT FILING DATE: 1999-05-17

PRIOR PILING DATE: 1999-05-18

NUMBER OF SEQ ID NOS: 145

SOFTWARE: PSESEE FOR Windows Version 4.0

SEQ ID NO 132

LENGTH: 10
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35;
      IndelB
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0
      0; Mismatches
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                                                                                                                                                                                               Sequence 3, Application US/09308984 Patent No. 6388065
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US-09-313-221A-132
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Matches 10; Conservative
        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AGCCAGCGAA 60
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                                                   51 AGCCAGCGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserva
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US-09-313-221A-132
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US-09-522-955A-3
                                                                                                                                                         RESULT 53
US-09-308-984-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Austin, Richard C.
APPLICANT: Hirsh, Jack
APPLICANT: Hirsh, Jack
APPLICANT: Weltz, Jeff
TITLE OF INVENTION: Methods and Compositions for Diagnosis
TITLE OF INVENTION: of Hyperhomocysteinemia
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                     13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 35; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%; Score 10; DB 1; 100.0%; Pred. No. 35;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
IS 111NG DATE: 03-JAN-1996
ATTORNEY/ACENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 016558-001200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                             05433/014001
PILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Fraet. Janis K.
FREGISTRATION NUMBER: 34,819
REPERENCE/DOCKET NUMBER: 05433
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

US-08-361-441B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/09016540; Patent No. 6132965; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AGCCAGCGAA 60
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Best Local Similarity
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 52
US-09-016-540-4
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STRANDEDNESS:
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                                               ## APPLICANT: 1am, occ ....
## APPLICANT: 1am, occ ....
## APPLICANT: 1al, Mindy
## APPLICANT: 1al, Mindy
## APPLICANT: 1al, Mindy
## APPLICANT: 6111, Stephen J.
## TITLE OF INVENTION: RINZ, A NOVEL INHIBITOR OF RAS-MEDICATED
## TITLE OF INVENTION: SIGNALING
## CURRENT APPLICATION NUMBER: US/09/522,955A
## CURRENT APPLICATION NUMBER: US/09/522,955A
## CURRENT APPLICATION NUMBER: US 08/942,819
## PRIOR PILING DATE: 1998-09-11
## PRIOR PILING DATE: 1997-10-02
## PRIOR PILING DATE: 1997-09-11
## PRIOR PILING DATE: 1997-09-11
## RIOR PILING DATE: 1997-09-11
## NUMBER OF SEQ ID NOS: 23
## SOFTWARE: PastSEQ for Windows Version 4.0
## SEQ ID NO 3
## LENGTH: 10
## TITLE OF THE OFFICE OFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 35; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Liang, Peng
APPLICANT: Dardee, Arthur B.
TITLE OF INVENTION: Messenger RNAs
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: ADDRESS:
ADDRESSER: Choate, Hall & Stewart
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02190

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US93/02246
FILING DATE: 19930311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Synthetic Oligonucleotide US-09-522-955A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Pasternack, Sam
REGISTRATION NUMBER: 29,576
REPERENCE/DOCKET UNBER: DFCI234CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 227-5020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/850,343
FILING DATE: 11-WAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617 227-7566
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
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STATE: Massachusetts
GENERAL INFORMATION:
APPLICANT: Tam, See-Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AGCCAGCGAA 60
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ZIP: 02190
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PCT-US93-02246-13
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WS-09-674-913B-14

Sequence 14, Application US/09674913B

Sequence 14, Application US/09674913B

Sequence 14, Application US/09674913B

Sequence 14, Application US/09674913B

Sequence 14, Application

APPLICANT: Gaddernack, Gustav

APPLICANT: Gaddernack, Gustav

APPLICANT: Gaddernack, Gustav

TITLE OF INVENTION: Their Use

TITLE OF INVENTION: Their Use

TITLE OF INVENTION: Their Use

FILE REFERENCE: 001702-401600

CURRENT APPLICATION NUMBER: US/09/674,913B

CURRENT FILING DATE: 1999-04-30

PRIOR FILING DATE: 1999-04-30

PRIOR FILING DATE: 1998-05-08

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin version 3.2

SEQ ID NO 14

LENGTH: 13
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Patent No. 5472843

GENERAL INFORMATION:
APPLICANT: Milliam, Curt L.
TITLE OF INVENTION: MCLERC ACID PROBES TO HAEMOPHILUS INFLUENZAE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 611 West Sixth Street
STREET: CA
STATE: CA
COUNTRY: USA
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                                                                                                                                             Score 10; DB 1; Length 10;
Pred. No. 35;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                   MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO PCT-US93-02246-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.0
Best Local Similarity 100.
Matches 10; Conservative
single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-221-968-2/c
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13.0%; Score 10; 100.0%; Pred. No.
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US-09-401-063-1837/c
; Sequence 1837, Application US/09401063
                                           Query Match 13.0
Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                     12 AGCGAAGCTG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                   55 AGCGAAGCTG
                                                                                                                                                                                                                             JS-08-985-162-1837/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-985-162-1837
       US-08-567-196-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: USA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,196
FILING DATE: 0-4-DEC-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US/08/567,196
FILING DATE: 25-APR-1991
ATPOREX/AGENT INFORMATION:
APPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 193/119
TELECOMMUNICATION INFORMATION:
TELEFRAX: 213-555-0440
TELEFRAX: 67-3510
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEBROTH: 14 bases
TYPE: nucleic acid
STRANDEDMESS: single
TERET TYPE: DNA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/690,788
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WALDLEY, RALDLAT ON
REFERENCE/DOCKET NUMBER: 193/119
TELEPHONE: 213-499-1600
TELEPHONE: 213-955-0440
TELEPHONE: 213-955-0440
TELEPHONE: 213-955-0440
TELEPHONE: 213-955-0440
TELEPHONE: APPLICATION: NUMBER: 193/119
TELEPHONE: 213-955-0440
TELEPHONE: 213-955-0440
TELEPHONE: 213-955-0440
TELEPHONE: APPLICATION: NUMBER: 193/119
TELEPHONE: 213-955-0440
TELEPHONE: 213-955-0440
TELEPHONE: APPLICATION: NUMBER: 193/119
TENGRIPHONESS: SINGLE
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AGCGAAGCTG 64
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                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA US-08-221-968-2
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US-08-567-196-2/c
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                                                                                                                                                                                                                                                 Sequence 1837, Application US/08985162
; Sequence 1837, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Abhtar; Saghir
APPLICANT: McSHip Patricia
APPLICANT: McSHip Patricia
TITLE OF INVENTION: GF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF REIDERMAL GROWTH
TITLE OF INVENTION: PACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Layon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
DB 1; Length 14; 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%; Score 10; DB 1; Length 14;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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1... 0; Mismatches
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 31.5" Diskette, 1.44 MD
MEDIUM TYPE: 91.5" Diskette, 1.44 MD
MEDIUM TYPE: 91.5" Diskette, 1.44 MD
MEDIUM TYPE: 91.5" DISKETTE, 1.00
COMEATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: FESTENG FOR WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REJERPONDISCATION NUMBER: 32,327
TELERPONDISCATION INFORMATION:
TELERPONDISCATION INFORMATION:
TELERPONT (213) 955-0440
INFORMATION FOR SEQ ID NO: 1837:
LENGTH: 14 base pairs
INFORMATION FOR SEQ ID NO: 1837:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
STRANDEDNESS: single
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US-08-867-820A-49/c
; Sequence 49, Application US/08867820A
Patent No. 589168;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
US-08-615-961-8
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GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Akhtar, Saghir
APPLICANT: Pell, Patricia
APPLICANT: Pell, Patric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.0%; Score 10; DB 1; Length 14;
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US-08-615-961-8
; Sequence 8, Application US/08615961
; Patent No. 5877162
; GENERAL INFORMATION:
    APPLICANT: Martina Werner and Shajl T. George
; TITLE OF INVENTION: Short External Guide Sequences
NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 2101 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                              ADDERSESE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUWTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: B.COMPUTER: 1.44 Mb
MEDIUM TYPE: B.COMPUTER: 0.05 S.0
SOFTWARE: PARESEQ for Windows 2.0
COMPUTER: IBM Compacible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PARESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/401,063
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY,AGENT INFORMATION:
NAME: WAAPULG, RICHARD 3.3237
REFERENCE/DOCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1837:
SEQUENCE CHARACTERISTICS:
LENGRICH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-401-063-1837
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APPLICANT: YAMGISHI Masahiro
APPLICANT: YAMGISHI Masahiro
APPLICANT: TAKAI Yukie
APPLICANT: TAKAI Yukie
APPLICANT: HARA Maxi
APPLICANT: HARA Maxi
APPLICANT: UEDA Makoto
APPLICANT: OHARA Akiko
TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S) - -HALOGENATED- -HYDROXYBUTY
NUMBER OP SEQUENCES:
ADDRESSEE: WENDEROIH, LIND & PONACK, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Weshington, D.C.
COUNTRY: USA
ZIP: 20006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,961
FILING DATE: THORDAMITION:
NAME: Pabbst, Patena L.
REGISTRATION NUMBER: 31,284
REFERRANCE/DOCKET NUMBER: 11,115
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION ON B:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR EQO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IDEN FC compatible
COMPUTER: IDEN FC COMPATIBLE
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,820A
FILING DATE: June 3, 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INPORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 1416/OP574US
TELECOMMUNICATION INPORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
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Sequence 1247, Application US/08679645
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                                                                                                                                                                                                                                                                     Gaps
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US-08-729-601A-7/C
i Sequence 7, Application US/08729601A
; Sequence 7, Application US/08729601A
; Patent No. 6166302
; GENERAL INFORMATION:
    APPLICANT: Merlo, Donald J.
    APPLICANT: Folkerts, Otto
    TITLE OF INVENTION: Lepidopteran Control in Plants
    NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Fitch, Even, Tabin & Flannery
    ADDRESSE: Fitch, Even, Tabin & Flannery
                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                        Query Match 12.7%; Score 9.8; DB 1; Length 13; Best Local Similarity 84.6%; Pred. No. 48; Matches 11; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60603
ZIP: 60603
EVENTURE READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,601A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isBE: Fitch, Even, Tabin & Flannery: 135 S. LaSalle St.
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 9.8; DB
84.6%; Pred. No. 48;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICALLO...
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Krueger, James P.
REGISTRATION NUMBER: 35,234
REFERENCE/DOCKET NUMBER: 60089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7848
TELEPAX: 312-372-7848
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
LENGTH: 13 base pairs
...... nucleic acid
                                                                           TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Selenophoma donacis
STRAIN: CBS417.51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / MOLECULE TYPE: DNA (genomic)
US-08-729-601A-7
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SEQUENCE CHARACTERISTICS
                   LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                          13 AGCTGATGACTTG 1
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Best Local Similarity
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                                                                                                                                                                                    US-08-867-820A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Gaps
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| Sequence 26, Application US/08233608 |
| Patent No. 5585238 |
| GENERAL INFORMATION: |
| APPLICANT: Ligon, James M |
| APPLICANT: Ligon, Detection of Fungal Pathogens Using the TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9.8; DB 1; Length 13;
Pred. No. 48;
0; Mismatches 2; Indels
APPLICANT: Zaick, Michael G.
APPLICANT: Zaick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: Edington, Brent E.
APPLICANT: Edingen, James A.
APPLICANT: Merlo, Patricia Ann Owens
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Polkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
CORRESPONDENCES: 1263
CORRESPONDENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: Suite 4700
CITTV: Los Accept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Call.
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE PORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: Unly 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: Unly 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY AGENT INFORMATION:
NAME: WASDLUGY RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 489-1600
TELER: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 1247:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: muclaic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%;
84.6%;
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Best Local Similarity 84.6'
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
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RESULT 65 US-08-679-645-1247/C

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 AAGCTGATGTCCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 AAGCTGGTGTTCT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-271-880A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Pred. No. 51;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bharat Chowira
APPLICANT: Bharat Chowira
APPLICANT: Bharat Chowira
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James D. Thompson
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,608
FILING DATE:
CLASSIPICATION NUMBER: US/08/233,608
FILING DATE:
NAME: Spruill, W. Marray
REGISTRATION NUMBER: 22,943
REFERENCE/DOCKET NUMBER: CGC 1739
TELEPHONE: 919-541-8615
TELEPHONE: 919-541-8615
TELEPHONE: 919-541-8615
TELEPHONE: 919-541-8615
TELEPHONE: HABBE PAIRE
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LYBE: NUCHEL acid
TYBE: Nucleic acid
TYBE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8corage
COMPUTER: BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOPTWARE: FastSEQ Version 1.5
                                        ADDRESSEB: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 67
US-08-271-880A-49/c
; Sequence 49, Application US/08271880A
; Patent No. 5693535
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AGACGGCCTGGGG 19
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NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
                                                                                  CITY: Hawth
STATE: NY
COUNTRY: UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-233-608-26
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CIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: DEP FC compatible
COMPUTER: DEP FC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,480
FILING DATE: US/08/887,480
FILING DATE: 15-OCT-1996
ATFORNEY/AGENT INPOMBER: US 08/722,187
FILING DATE: 15-OCT-1996
ATFORNEY/AGENT INPOMBER: US/08/887,487
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
APPLICATION UNDER: US/08/271,880A
FILING DATE: July 7, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/103,243
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
APPLICATION NUMBER: 32,327
REFERENCE WATHORNATION:
NAME: WAZDUTE, RICHARA
REGISTRATION NUMBER: 32,327
REFERENCE POCKET NUMBER: 32,327
REFERENCE (213) 489-1600
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION OF SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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0; Mismatches
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Sequence 62, Application US/08485689
Fatent No. 5855408:
GENERAL INFORMATION:
APPLICANT: Hampel, Arnold E.
APPLICANT: Tritz, Richard H.
TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATES: New York
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MEDIUM TYPE: Floppy disk
COMPUTER: ERLOPPY disk
COMPUTER: IBM FC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,689
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 43863-CIX/JPW/KJP
TELEPHONE: 212-278-4400
               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.7%; Score 9.8; DB
84.6%; Pred. No. 51;
tive 0; Mismatches
                                                                                                                                                                                        Query Match 12.7%; Score 9.8; DE Best Local Similarity 84.6%; Pred. No. 51; Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
: United States Of America
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US-08-476-021A-62/c
S. Sequence 62, Application US/08476021A
; Patent No. 5858785
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // MOLECULE TYPE: RNA (genomic)
US-08-485-689-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-278-0526
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               7 AGACGGCCTGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAACAAGACGGCC 14
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 AAACAGGACGGTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                          ; ANTI-SENSE: NO
US-08-887-480-26
                                                                                                      HYPOTHETICAL:
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| Patent No. 5869339
| GENERAL INFORMATION:
| APPLICANT: Hampel, Arnold B.
| APPLICANT: Tritz, Richard H.
| TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                  RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
APPLICANT: Hampel, Arnold E.
APPLICANT: Tritz, Richard H.
TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STRATE: New York
COUNTRY: United States Of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATING SYSTEM: O7-JUN-1995
CLASSIFICATION NUMBER: US/08/476,021A
PILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REFERRINGE/DOCKET NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REFERRINGE/DOCKET NUMBER: 28,678
REFERRINGE/DOCKET NUMBER: 212-278-040
TELERHONE: CONTENTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESESE: Cooper & Dunham LLP
STRET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States Of America
ZIP: 10036
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Disk PC-OMPSIA-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,608B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPOMENTION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 84.67
Matches 11, Conservative
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13 AGACGGCCTCCGG 1
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US-08-910-408-49
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                                                                                                                                                    JS-08-910-408-49/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 72
US-08-722-187-26/C
i Sequence 26, Application US/08722187
i Sequence 25, Application US/08722187
j Patent No. 5952374
j GENERAL INPORMATION:
i APPLICANT: 119cn, James M
i APPLICANT: 119cn, James M
i TITLE OF INVENTION: Detection of Fungal Pathogens Using the TITLE OF INVENTION: Polymerase Chain Reaction
i NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
i ADDRESSEE: Clba-Geigy Corporation
STREET: 7 Skyline Drive
i CITY: Hawthorne
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                                                                                                                                                                                                                                                                                DB 1; Length 14;
                                                                                                                                                                                                                                                                                                                          2; Indels
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ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,187
    43863-C1Z/JPW/KJP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other nucleic acid
Oligonucleotide primer JB443
                                                                                                                                                                                                                                                                              12.7%; Score 9.8;
84.6%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSISTICATION: 435
CLASSISTICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-866
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: NUCleic acid
STRANDENNES: single
REFERENCE/DOCKET NUMBER: 4:
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-278-0400
                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)

US-08-478-608B-62
                                                           TELEFAX: 212-278-0526
INPORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                  2 AAACAÁGACGGCC 14
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.6
Matches 11; Conservative
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MOLECULE TYPE: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                APPLICANT: Reneth G. Draper
APPLICANT: Bharat Chowrira
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: James D. Thompson
TITLE OF INVENTION: HUMAN IMMUNODEPICIENCY VIRUS
TITLE OF INVENTION: HUMAN IMMUNODEPICIENCY VIRUS
TITLE OF INVENTION: REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 14;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: PastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,408
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/271,880
FILING DATE: July 7, 1994
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WATCHING, RICHARD
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1769, Application US/08985162; Patent No. 6057156
Sequence 49, Application US/08910408
Patent No. 5972704
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%;
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELERAX: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.7
Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                           STREET: Suite 4700
CITY: Los Angeles
STATE: California
CONTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
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US-08-476-423A-62/C

US-08-476-423A-62/C

Sequence 62, Application US/08476423A

Patent No. 621661

GENERAL INFORMATION:

APPLICANT: Hampel, Arnold B.

APPLICANT: Tritz, Richard H.

TITLE OF INVENTION: RAN CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES:

NUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

COUNTRY: United States Of America

ZIP: 10036

CONFUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Day disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

PILING DATE: 07-JUN-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.7%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 51; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                             COMPUTER: IBM COMPACIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARRE: FRANCESCOVERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,408
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 08/10,408
FILING DATE: AUGUST 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: AUGUST 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: AUGUST 6, 1993
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INPORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
TELECOMMUNICATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 49: US-09-249-215-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                storage
                      STATE: California
COUNTRY: U.S.A.
ZIP: 90071
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Bharat Chowrira
James McSwiggen
Dan T. Stinchcomb
James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
HUMAN IMMUNDEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 14;
                 APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James Applicant: McSwiggen, James Applicant: McSwiggen, James Applicant: McSwiggen, James Applicant Action of Diseases or Conditions Related Title OF INVENTION: TO LEVELS OF REIDERWAL GROWTH TITLE OF INVENTION: FACTOR RECEPTORS NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 613 Weet Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 9.5" Diskette, 1.44 Mb
MEDIUM TYPE: 9.5" Diskette, 1.44 Mb
MEDIUM TYPE: 13.5" Diskette, 1.44 Mb
MEDIUM TYPE: 13.5" Diskette, 1.44 Mb
MEDIUM TYPE: 14.0 COMPUTER: 18M COMPAGE
OPERATING SYSTEM: 18M P.C. DOS 5.0
SOFTWARE: PARENEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05.40
FILING DATE: 04 December 1997
CLASSIFICATION STAR: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 33,327
RELEPAN: (213) 489-1600
TELLERA: 67-3510
INFORMATION FOR SEQ ID NO: 1769:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
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CORRESPONDENCE ADDRESSE: Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPLICATION
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Patent No. 6159692
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 4700
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EDNESS: single
                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
GENERAL INFORMATION:
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US-09-249-215-49/c
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Gaps ö

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Sequence 99, Application US/09135020

Sequence 99, Application US/09135020

Sequence 99, Application US/09135020

GENERAL INFORMATION:
APPLICANT: Seating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Salawaki, Igor
ITILE OF INVENTION: WUTATIONS IN THE KCNE1 GENE ENCODING HUMAN mink WHICH
ITILE OF INVENTION: WUTATIONS IN THE KCNE1 GENE
TITLE OF INVENTION: KCNE1 AN LOT GENE
FILE REPERENCE: 2323-131
CURRENT APPLICATION NUMBER: 08/921,068
SARLIER APPLICATION NUMBER: 08/921,068
SARLIER PILING DATE: 1998-08-17
SARLIER PILING DATE: 1996-10-29
SARLIER PILING DATE: 1996-10-29
SARLIER APPLICATION NUMBER: 60/019,014
SARLIER PILING DATE: 1998-07-29
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Pred. No. 51;
0; Mismatches 2; Indels
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                              43863-C2/JPW/KJP
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Pred. No. 51;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 99, Application US/09135010A
Patent No. 6277978
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Landes, Gregory M.
APPLICANT: Landes, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 4386
TELECOMMUNICATION INFORMATION:
TELEPHONB: 212-278-0400
TELEPAX: 212-278-0526
INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%;
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84.6%;
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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ORGANISM: Homo sapiens
US-09-135-020-99
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            US-08-476-423A-62
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US-09-373-845-19
Sequence 19, Application US/09373845
Sequence 19, Application US/09373845
Sequence 19, Application US/09373845
GREENL INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 4468 US
CURRENT APPLICATION NUMBER: US/09/373,845
CURRENT PILLING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 99, Application US/09444871

Betent No. 6323026

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Keating, Mark T.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Splawski, Igor

APPLICANT: Splawski, Igor

TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THERBY ESTABLISHING

TITLE OF INVENTION: CCNEI AS AN LQT GENE

FILE REPERENCE: 2323-131

CURRENT APPLICATION NUBER: US/09/444,871

CURRENT FILING DATE: 1999-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 14;
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APPLICANT: Splawski, igor
TITLE OF INVENTION: KVLQT1 - A LONG OT SYNDROME GENE
FILE REFERENCE: 2323-133
CURRENT APPLICATION NUMBER: US/09/135,010A
CURRENT APPLICATION NUMBER: 60/094,477
PRIOR PPLICATION NUMBER: 60/094,477
PRIOR PILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 08/321,068
PRIOR PILING DATE: 1998-07-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-11-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PATENTIN UNF. 2.0
SOFTWARE: PATENTIN VOT: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9.8; DB 1;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9.8; DB Pred. No. 51; 0; Mismatches
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Best Local Similarity 84.6%;
Matches 11; Conservative (
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Best Local Similarity 84.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Unknown Organism FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ACAAGACGGCCTG 16
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                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-135-010A-99
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RESULT 84
US-09-597-732-99
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US-09-081-646-24

i Sequence 24, Application US/09081646

j Sequence 24, Application US/09081646

j Patent No. 6333152

i GENERAL INFORMATION:

j APPLICANT: Kinzler, Kenneth

j APPLICANT: Zhang, Lin

APPLICANT: Zhang, Lin

j TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

TITLE OF INVENTION: Cancer Cells

FILE REPRENCE: 0100.74664

CURRENT APPLICATION NUMBER: US/09/081,646

CURRENT APPLICATION NUMBER: US/09/081,646

SARLIER PILING DATE: 1998-05-20

SARLIER PILING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 871

SOFTWARE: PASESEQ for Windows Version 3.0

SEQ ID NO 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.7%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 51; Matches 11; Conservative 0; Mismatches 2; Indels
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US-09-597-735-99
; Sequence 99, Application US/09597735
; Patent NO. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Banguinetti, Michael C.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 9.8; DE 84.6%; Pred. No. 51; tive 0; Mismatches
EARLIER APPLICATION NUMBER: US 09/135,020
EARLIER FILING DATE: 1998-08-17
EARLIER FILING DATE: 1998-08-17
EARLIER FILING DATE: 1997-08-29
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 08/739,383
EARLIER APPLICATION NUMBER: 60/019,014
EARLIER FILING DATE: 1995-10-22
EARLIER FILING DATE: 1995-12-22
EARLIER FILING DATE: 1998-07-29
MUMBER OF SEQ ID NOS: 114
SOFTWARE: PALENTIN VOT: 2.0
SEQ ID NO 99
LENGTH: 14
            APPLICATION NUMBER: US 09/135,020
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-09-081-646-24
                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-871-99
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, 1gor
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
FILLE OF INVENTION: MUMBER: 09/135,020
PRIOR FILLING DATE: 1998-08-17
PRIOR FILLING DATE: 1998-08-17
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-12-22
PRIOR FILING DATE: 1995-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
SOFTWARE: PATCHING DATE: 1998-07-29
SEQ ID NO 99
LENGTH: 14
TANDER OF SEQ ID NOS: 114
TANDER OF SEQ ID NOS: 114
TANDER OF SEQ ID NO 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9.8; DB 1; Length 14;
Pred. No. 51;
0; Mismatches 2; Indels
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Pred. No. 51;
0; Mismatches 2; Indels
                   CURRENT FILING DATE: 2000-06-19
REARLIER PEDICATION NUMBER: 09/135,010
EARLIER APPLICATION NUMBER: 00/94,477
EARLIER APPLICATION NUMBER: 06/094,477
EARLIER APPLICATION NUMBER: 08/921,068
EARLIER PILING DATE: 1999-07-29
EARLIER PEDICATION NUMBER: 08/739,383
EARLIER PELING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: 06/019,014
EARLIER APPLICATION NUMBER: 06/019,014
EARLIER PILING DATE: 1995-12-22
SEQID NOS: 116
SEQID NO 99
APPLICATION NUMBER: US/09/597,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application US/09444295
Patent No. 6432644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.7%;
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-597-735-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
US-09-444-295-99
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DB 1; Length 14;

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US-09-401-063-1769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sanguinetti, Michael C.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark T.
APPLICANT: Curran, Mark T.
APPLICANT: Curran, Mark T.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: Burn, Wighter, US/09/597,731
CURRENT APPLICATION NUMBER: 09/135,010
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR PILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 99
IENGTH: 14
                                                             JOURNAGOUL INFORMATION:
JOURNAGOUL INFORMATION:
JAPPLICANT: Sanguinetti, Michael C.
JAPPLICANT: Curran, Mark E.
JAPPLICANT: Curran, Mark E.
JAPPLICANT: Cunnors, Timothy D.
JAPPLICANT: Connors, Timothy D.
JAPPLICANT: Burn, Timothy C.
JAPPLICANT: Burn, Timothy C.
JAPPLICANT: Bolawski, Igor
JITLE REFERENCE: 2323-133
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/135,010
PRIOR PILING DATE: 1998-00-17
PRIOR PILING DATE: 1998-07-29
PRIOR PILING DATE: 1998-07-29
PRIOR PILING DATE: 1997-08-29
PRIOR PILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR PILING DATE: 1995-10-29
PRIOR APPLICATION NUMBER: 60/19,014
PRIOR APPLICATION NUMBER: 60/19,014
PRIOR PILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 99
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9.8; DB
Pred. No. 51;
0; Mismatches
Sequence 99, Application US/09597732
Patent No. 6451534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 99, Application US/09597731; Patent No. 6582913; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-09-597-732-99
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CRGANISM: Homo sapiens
US-09-597-731-99
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Patent No. 6623962

GENERAL INCRNATION:
GENERAL INCRNATION:
APPLICANT: RAHLARY Saghir
APPLICANT: RAMARINE SAGHIR
APPLICANT: RASWAGEN, James
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: PACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 63164 4700
CITY: LOS Angeles
STATE: California
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 14;
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Pred. No. 51;
0; Mismatches
Query Match
12.7%; Score 9.8; DE
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Computer; 1.00 COMPUTER: 10 COM
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,162
FILING DATE: 04 December 1997
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 230/107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHORE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-04712-26/c
; Sequence 26, Application PC/TUS9504712
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TELEX: 67-3510
INPORMATION FOR ESC ID NO: 1769:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.7%;
Best Local Similarity 84.6%;
Matches 11; Conservative
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TYPE: DNA ORGANISM: Artificial Sequence ORGANISM: FEATURE: OTHER INFORMATION: Synthetic
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ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-173-489C-331
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US-09-940-244-415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                APPLICANT: Ligon, James M
APPLICANT: Ligon, James M
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
TITLE OF INVENTION: Polymerase Chain Reaction
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSES: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 14;
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US-08-173-489C-331
| Sequence 331, Application US/08173489C
| Patent No. 5861244
| GENERAL INFORMATION:
| APPLICANT: WANG, C. -G. |
| TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORWATION. |
| TITLE OF SEQUENCES: 365 |
| CORRESPONDENCE ADDRESS: 365 |
| ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                            ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDMENT.
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Oligonucleotide primer JB443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%; Score 9.8; DE 84.6%; Pred. No. 51; tive 0; Mismatches
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ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                                                              PILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY, AGENT UNFORMATION:
NAME: Walsh, Andrea C
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: GGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFRAX: 919-541-8666
TELEFRAX: 919-541-8669
TELEFRAX: 919-541-8669
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AGACGGCCTGGGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 11; Conser
GENERAL INFORMATION:
                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO PCT-US95-04712-26
                                                                                                                                                                                                                       STATE: NY COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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DESCRIPTION: 16s TRNA gene from Neisseria
DESCRIPTION: genorrhoeae (Accession # X07714) nucleotides
DESCRIPTION: 189 to 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE: Nucleotide sequence of a 16s
TITLE: Incommal RNA gene from Neisseria gonorrhoeae
JOURNAL: Nucleic Acids Research
VOLUME: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 331 :FROM 1 TO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 415, Application US/09940244

Patent No. 6692917

GENERAL INPORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Application Dendrimers
FILE REFERENCE: FORS-06478

CURRENT APPLICANT: RORS-06478

CURRENT PAPLICANTON NUMBER: US/09/940,244

CURRENT PILING DATE: 2002-05-06

NUMBER OF SEQ ID NOS: 422

SOFTWARE: PatentIn version 3.1

LENGTH: 12
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTONEV/AGENT INFORMATION:
NAME: HANGHIMAN, JOSEPH H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEFAN: (attorney) (212) 708-1880
TELEFAN: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 331:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TEMPER HUGGE acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Neisseria gonorrhoeae
STRAIN: NCTC 83785.
PUBLICATION INFORMATION:
AUTHORS: Roseau, R, Heyndrickx, L,
AUTHORS: Heuverswyn, H.
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US-08-471-973A-26/c

Sequence 26, Application US/08471973A

Sequence 26, Application US/08471973A

Patent No. 5872232

GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: Andrew Kawasaki
ITLE OF INVENTON: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
             US-08-468-037A-26/c

US-08-468-037A-26/c

Sequence 26, Application US/08468037A

Sequence 26, Application US/08468037A

Sequence 26, Application

Sequence 26, Application

Patron Normal Sequence 37

CORRESPONDRICE ADDRESS:

ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris

STREET: One Liberty Place - 46th Ploor

CITY: Pilladelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
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                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,037A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 815,932
FILING DATE: 05-MR-1992
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH LUCCI
REGISTRATION NUMBER: 33,307
REFERENCE/POCKET NUMBER: 1515-2004
TELLERDHORE: 215-568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERICES:
LENGTH: 13 bases
LENGTH: 13 bases
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MEDIUM TYPE: 3.5 inch disk, 720 KD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AGACGGCCTGG 17
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-468-037A-26
                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 19103
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NAME/KEY: misc_feature

LOCATION: (4)...(4)

OTHER INFORMATION: The residue at this position is linked to a spacer bearing a Cy3

OTHER INFORMATION: dye.
US-09-940-244-415
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US-08-738-944-39
; Sequence 39, Application US/08738944
; Patent No. 5783431
; GENERAL INFORMATION:
; TITLE OF INVENTION: METHODS FOR GENERATING AND
; TITLE OF INVENTION: SCREENING NOVEL METABOLIC PATHWAYS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STRRET: 1155 Avenue of the Americas
; CITY: New York
                                                                                                                              Score 9.4; DB 1; Length 12; Pred. No. 52; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9.4; DB 1; Length 13;
Pred. No. 55;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREESEQ Version 2.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/738,944
FILING DATE: 24-CT-1996
CLASSIPICATION DATE: 356
FILING DATE: 24-DR-1996
APPLICATION NUMBER: USSN 08/639,255
FILING DATE: 24-DR-1996
APPLICATION NUMBER: USSN 08/639,255
FILING DATE: 24-DR-1996
APPLICATION NUMBER: USSN 08/639,255
FILING DATE: 24-DR-1996
ATTORNEY/AGENT INPORMATION:
NAME: COTUZZI, LAURA A
REGISTRACE/DOCKET NUMBER: 8757-007
FILERPHONE: 212-90-90
TELERPHONE: 212-90-90
TELERPHONE: 212-90-90
TELERPHONE: 212-90-90
TELERPHONE: 212-90-90
TELERPHONE: 212-869-8864
INPORMATION POR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: mucleic acid
STERANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 5...6
OTHER INFORMATION: pDblet Vector
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90.9%;
                                                                                                                                12.2%;
90.9%;
                                                                                                                              Query Match
Best Local Similarity 90.5
Matches 10; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-738-944-39
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Sequence 30, Application US/09263352

Sequence 30, Application US/09263352

Patent No. 624211

GENERAL INFORMATION:

APPLICANT: Peterson, T.

APPLICANT: Brian, P.

TITLE OF INVENTION: METHODS FOR GENERATING AND SCREENING NOVEL METABOLIC

TITLE OF INVENTION: PAHWAYS

TITLE OF INVENTION: PAHWAYS

FILE REFERENCE: 8757-010

CURRENT APPLICATION NUMBER: US/09/263,352

CURRENT FILING DATE: 1999-03-05

RARLIER FILING DATE: 1997-12-05

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08936166A

Fatent No. 6307040

GENERAL INFORMATION:

APPLICANT: Cook, Phillip Dan

APPLICANT: Advasaki, Andrew M

TITLE OF INVENTION: Modilate Gene Expression

FILE OF INVENTION: Modilate Gene Expression

FILE REFERENCE: 16182708

CURRENT APPLICATION NUMBER: US/08/936,166A

CURRENT APPLICATION NUMBER: 07/835,932

EARLIER PILING DATE: 1992-03-05

NUMBER OF SEQ ID NOS: 12

SOFTWARE PLANCE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-263-352-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Combined DNA/RNA Molecule: OTHER INFORMATION: Artificial Sequence
                                                                                                          12.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 55; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%; Score 9.4; DB 1; Length 13; 90.9%; Pred. No. 55; 1; Indels :ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 9.4; DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                  Query Match
Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                          7 AGACGGCCTGG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 94
US-09-263-352-30
                                            US-09-035-357-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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US-09-035-357-26/c
; Sequence 26, Application US/09035357
; Sequence 26, Application US/09035357
; Patent No. 6005087
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBERS OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,973A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 835,932
FILING DATE: 05-MAR.1992
ATTORNEY, AGENT INFORMATION:
NAME: JOSEPH LUCCH
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION 
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/468,037
PRIOR APPLICATION NUMBER: 08/468,037
FILING DATE:
ATTONNEY AGENT INFORMATION:
NAME: JOSEPH LUCCI
REFIRENCE/DOCKET NUMBER: 151S-2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 315-568-3100
TELEPHONE: 315-568-3100
TELEPHONE: 315-568-3100
TELEPHONE: 315-568-3100
TELEPHONE: 315-568-3100
TELEPHONE: 315-568-3100
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 KD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-471-973A-26
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Gaps

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Query Match
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US-09-135-202-26/c

Sequence 26, Application US/09135202

Sequence 26, Application US/09135202

Sequence 26, Application US/09135202

Patent No. 6399754

GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: Phillip Dan Cook
APPLICANT: Sugar Modified Oligonucleotides

TILLS OF INVENTION: 37

CORRESPONDENCES: 37

CORRESPONDENCES: Weahburn Kurtz Mackiewicz and No. 6399754ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia
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                      1; Indels
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Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 141, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribosyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Bendin, Amber
; APPLICANT: Randry, Amber
; APPLICANT: Karpeisky, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH LUCCI
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 15IS-2005
TELEFONMULCATION INFORMATION:
TELEFONDE: 215-568-3100
TELEFONS: 215-568-3100
TELEFONS: 215-568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 19103
COMPUTER READABLE FORM:
COMPUTER: 15 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,202
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%;
90.9%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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Adamic, Jasenka
Sweedler, David
Zinnen, Shawn
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; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-135-202-26
                                                         7 AGACGGCCTGG 17
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                                                                                              12 AAACGGCCTGG 2
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Best Local Similarity
Matches 10; Conserva
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot PILE REPERENCE: MBHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US 60/094,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR PILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SEQ ID NO 141
LENGTH: 13
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Patent No. 6531584

GENERAL INFORMATION

APPLICANT: Phillip Dan Cook

APPLICANT: A. Kawasaki

ITILE OF INVENTION: 2' Modified Oligonucleotides

TITLE OF ENGURENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6531584ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia
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90.9%; Pred. No. 55;
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APPLICATION NUMBER: US/09/389,283
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/035,357
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: JOSEPH LUCCI
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 1515-2004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: 215-568-3100
TELERAX: 315-368-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.2
Best Local Similarity 90.9
Matches 10; Conservative
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US-09-474-432B-141
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US-09-389-283-26
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US-09-389-283-26/c
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APPLICANT: Rarpeisky, All Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nuclectide Triphosphate and their Incorporation into Oligonucleot
FILE REFERENCE: MBHB00-831-C (249/073)
CURRENT PELLING DATE: 2001-04-04
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SSEQ ID NO 141
LENGTH: 13
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                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Perlagen Sciences, Inc.
APPLICANT: Cox, David R
APPLICANT: Cox, David R
APPLICANT: Margus, Bradley A
TITLE OF INVENTION: GENETIC ANLYSIS SYSTEM AND METHODS
TITLE OF TRENT SPLICATION NUMBER: US/10/042,819
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 13
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                    1; Indels
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Pred. No. 55;
0; Mismatches
Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
; OTHER INFORMATION: HYPOTHETICAL SEQUENCE
US-10-042-819-8
                                                                                                                                                                                                                                                       APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
                                                                                                                                                                                                Sequence 141, Application US/09476387; Patent No. 6617438; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10042819; Patent No. 6897025; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
Best Local Similarity 90.9%;
Matches 10; Conservative
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Best Local Similarity 90.5
Matches 10; Conservative
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                                                         7 AGACGGCCTGG 17
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                                                                                | ||||||||
12 AAACGGCCTGG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
ORGANISM: Homo sapiens
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US-10-042-819-8/c
                                                                                                                                                            RESULT 99
US-09-476-387-141
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Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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46 TAAAGAGCCAG 56 |||||||||| 12 TAAAGAGTCAG 2 Search completed: April 19, 2006, 16:10:20 Job time : 0.001 secs

25-MAY-2001; 2001US-00865866.

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The present invention describes a compound (1) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR), coding, a 'UTR or introp'region of a nucleic acid molecule encoding phospholipase A2, group IIA (synovial), where the compound specifically hybridises with and inhibits the expression of phospholipase A2, group IIA (synovial).

Also described: (1) a composition comprising the compound and carrier or diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues; and (3) a method of treating an animal straing a disease or condition associated with phospholipase A2, group IIA (synovial). (1) has antinflammatory, antidabetic, cytostatic and antipsoriatic activities, and can be used in vaccines and in gene therapy. The compound (1) can be used for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represents a human phospholipase A2 group IIA (synovial). (2) the compound (1) can be used for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represents a human phospholipase A2 group IIA (synovial) contact the present sequence represents a human phospholipase A2 group IIA (synovial) contact is present sequence the present in an antipense oligonucleotide, which is used in an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                  New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.0%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        example from the present invention
                                                                                                                  Claim 3; Page 86; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 CTCTGAGAGGTAAAGAGCCA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCTGAGAGGTAAAGAGCCA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC46925 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis; diabetes; ss.
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WPI; 2003-140495/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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The present invention describes a compound (I) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR), coding, 2' UTR or intron region of a nucleic acid molecule encoding phospholipase A2, group IIA (synovial), where the compound specifically hybridises with and inhibits the expression of phospholipase A2, group IIA (synovial).

Also described: (1) a composition comprising the compound and a carrier of diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with phospholipase A2, group IIA (synovial). (I) has antinflammatory, antidiabetic, cytostatic and antipporiatic activities, and can be used in vaccines and in gene therapy. The compound (I) can be used for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represents a human phospholipase A2 group IIA (synovial) composition to the present sequence represents a human phospholipase A2 group IIA (synovial) composition to the present sequence represents a human phospholipase A2 group IIA (synovial)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                             New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.
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/note= "2'-O-methoxyethyl (2'-MOE) gapmer"
16. .20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 86; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 GTCCTCTGAGAGGTAAAGAG 52
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/mod_base= OTHER
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/*tag= b
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                                                                                                 (ISIS-) ISIS PHARM INC.
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/*tag=
                                                                                                                                                                Bennett CF, Wyatt JR,
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Matches
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ACC46922/c
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or diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with phospholipase A2, group IIA (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and antipsoriatic activities, and can be used in vaccines and in gene therapy. The compound (I) can be used for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represents a human phospholipase A2 group IIA (synovial) chimeric phosphorothloate, antisense oligonucleotide, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                       Phospholipase A2 group IIA; synovial; antisense modulation; inflammation; phospholipase A2 group IIA inhibitor; phosphorothicate; antiinflammatcry; antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer; psoriasis; diabetes; se.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                               Human phospholipase A2 antisense oligonucleotide SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gapmer
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                                                                                                                                                                               Score 20; DB 1; Length 20;
Pred. No. 6.7;
                                                                                                                                                                                                         0; Indels
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/note= "2'-O-methoxyethyl (2'-MOE)
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                                                                                                                                                     Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                         0; Mismatches
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                                                                                                                           example from the present invention
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/mod_base=
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modified_base
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Example 15; Page 86; 135pp; English

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The present invention describes a compound (I) comprising 8-50
nucleobases which is targeted to a 5' untranslated region (UTR), coding,
3' UTR or intron region of a nucleic acid molecule encoding phospholipase
A2, group IIA (synovial), where the compound specifically hybridises with
and inhibits the expression of phospholipase A2, group IIA (synovial).
Also described: (1) a composition comprising the compound and a carrier
or diluent; (2) a method of inhibiting the expression of phospholipase
A2, group IIA in cells or tissues, and (3) a method of treating an animal
having a disease or condition associated with phospholipase A2, group IIA
(synovial). (1) has antiinflammatory, antidiabetic, cytostatic and
antipsoriatic activities, and can be used in vaccines and in gene
therapy. The compound (I) can be used for preparing a composition for
treating or preventing inflammation, cancer, psoriaals or diabetes. The
present sequence represents a human phospholipase A2 group IIA (synovial)
chimmeric phosphorothioate antisense oligonucleotide, which is used in an
example from the present invention
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Pred. No. 6.7;
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/note= "2'-O-methoxyethyl (2'-MOE)
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                                                                                                                                                                                                                                                                                          Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;
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/*tag= a
/mod_base= OTHER
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100.0%;
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Best Local Similarity 100...
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nucleobases which is targeted to a 5' untranslated region (UTR), coding,
and include the expression of a nucleic acid molecule encoding phospholipase
A2, group IIA (synovial), where the compound specifically hybridises with
and inhibits the expression of phospholipase A2, group IIA (synovial).
Also described: (1) a composition comprising the compound and a carrier
or diluent; (2) a method of inhibiting the expression of phospholipase
A2, group IIA in cells or tissues; and (3) a method of treating an animal
adjaces or condition associated with phospholipase A2, group IIA
(synovial). (I) has antiinflammatory, antidiabetic, cytosteric and
antipsoriatic activities, and can be used in vaccines and in gene
therapy. The compound (I) can be used for preparing a composition for
treating or preventing inflammation, cancer, postasis or diabetes. The
present sequence represents a human phospholipase A2 group IIA (synovial)
chimeric phosphorothioate antisense oligonucleotide, which is used in an
example from the present invention
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                                                                                                                                                                                               New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.
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/note= "2'-0-methoxyethyl (2'-MOE) gapmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAAACAAGACGGCCTGGGGA 20
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/mod_base= OTHER
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                                                                         21-MAY-2002; 2002WO-US016135.
                                                                                                25-MAY-2001; 2001US-00865866.
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                                                                                                                        (ISIS-) ISIS PHARM INC
                                                                                                                                                 Bennett CF, Wyatt JR,
                                                                                                                                                                        WPI; 2003-140495/13.
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ACC46924/c
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The present invention describes a compound (I) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR), coding, 3' UTR or intron region of a nucleic acid molecule encoding phospholipase A2, group IIA (synovial), where the compound specifically hybridises with and inhibits the expression of phospholipase A2, group IIA (synovial).

Also described: (1) a composition comprising the compound and a carrier or diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with phospholipase A2, group IIA (synovial). (1) has antinflammatory, antidiabetic, cytostatic and antipsorlatic activities, and can be used in vaccines and in gene therapy. The compound (1) can be used for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes. The present sequence represents a human phospholipase A2 group IIA (synovial). Chimeric phosphorchioate antisense oligonucleotide, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psorlasis or diabetes.
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                                                                                  16.20
/*tag= c
/mod bage= OTHER
/note= "2'-0-methoxyethyl (2'-MOE) gapmer"
/mod_base= OTHER
/note= "2'-O-methoxyethyl (2'-MOB) gapmer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7;
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Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 CAACTCTGGAGTCCTCTGAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 CAACTCTGGAGTCCTCTGAG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2001; 2001US-00865866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2002; 2002WO-US016135
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06-JAN-2005
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                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a compound (I) comprising 8-50 nucleobases which is targeted to a 5' untranslated region (UTR), coding, 3' UTR or intron region of a nucleic acid molecule encoding phospholipase C 3' UTR or intron region of a nucleic acid molecule encoding phospholipase C and inhibits the expression of phospholipase A2, group IIA (synovial).

Also described: (1) a composition comprising the compound and a carrier or diluent; (2) a method of inhibiting the expression of phospholipase A2, group IIA in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with phospholipase A2, group IIA (synovial). (I) has antiinfilammatory, antidiabetic, cytostatic and can be used in vaccines and in gene therapy. The compound (I) can be used for preparing a composition for treating or preventing inflammation, cancer, psoriaats or diabetes. The present sequence represents a human phospholipase A2 group IIA (synovial) chimeric phosphorothioate antisense oligonucleotide, which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                      Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.
                                                                                                                                                                                                                                                                                                                                           compound that hybridizes with and inhibits the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                    /*tag= c
/mod_base= OTHER
/note= "2'-0-methoxyethyl (2'-MOE) gapmer"
                                                                                                              /note = "2'-0-methoxyethyl (2'-MOE) gapmer"
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                                                                   /note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDH6 siRNA antisense sequence, SEQ ID 6072.
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 86; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 GCCTGGGGATACAACTCTGG 31
                                                       /mod_base= OTHER
                                                                                                   /mod_base= OTHER
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                                                                                                                                                                                                                                                   25-MAY-2001; 2001US-00865866
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nes 20; Conservative
                                                                                                                       16. .20
                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                Bennett CF, Wyatt JR;
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                                                                                                                                                                                 WO200297133-A1
                               modified base
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                                                                                                                        modified_base
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                                                                                                                                                                                                      05-DEC-2002
Synthetic
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The present invention relates to a novel pharmaceutical composition

comprising: (a) an agent capable of modulating an expression level or

protein activity of a cancer-related transmembrane protein (CRTP) or gene

an antibody specific for a CRTP, or a T cell activated by a CRTP; and

(b) a carrier. The pharmaceutical composition may also comprise a

colymucleotide capable of inhibiting or decreasing the expression of the

CRTP by RNA interference or an antisense mechanism. The CRTPs of the

chromotion are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3,

convertion are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3,

convertion are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3,

convertion are selected from a useful for treating cancer, e.g. colon

cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney

cancer, stomach cancer, and esophageal cancer. The present sequence is a

CRTP short interfering RNAS (siRNA) oligonucleotide. Note: The sequence

data for this patent did not form part of the printed specification, but

was obtained in electronic format directly from WIPO at

[tp.wipo.int/pub/published_pct_sequences]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
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Cytostatic, Gene therapy, Vaccine, RNA Interference, cancer, 88; short interfering RNA, gene silencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 3 A; 6 C; 5 G; 0 T; 7 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 6072; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOWER SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 AAGAGCCAGCGAAGCTGATGT 68
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                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2004; 2004WO-US015645.
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Best Local Similarity
Matches 19; Conserval
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                                                                                                                                                                                                                         WO2005001092-A2
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                                                                                                                                                                                          The present invention relates to a novel pharmaceutical composition

comprising: (a) an agent capable of modulating an expression level or

protein activity of a cancer-related transmembrane protein (GRTP) or gene
; an antibody specific for a CRTP, or a T cell activated by a CRTP; and

(b) a carrier. The pharmaceutical composition may also comprise a
polynucleotide capable of inhibiting or decreasing the expression of the

CRTP by RNA interference or an antiseane mechanism. The CRTPs of the
invention are selected from ABC4, C20orf103, CACNAID, CDH6, CST, ENPP3,

FLJ1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
pharmaceutical composition is useful for treating cancer, e.g. colon
cancer, stomach cancer, breast cancer, prostate cancer, liver cancer, kidney
cancer, stomach cancer, not esophageal cancer. The present sequence is a
target oligonucleotide from one such CRTP for which short interfering
CRNAB (aiRNA) were produced. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at

Etp. wipo.int/pub/published_pot_sequences
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                                                                                                                Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                               21.8%; Score 16.8; DB 1; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 6 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDH6 target oligonucleotide, SEQ ID 5566.
                                                                                                                                                                        Claim 3; SEQ ID NO 6070; 113pp; English.
                                                                    Howes SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Be X, Wei L, Slonim DK, Howes SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AGAGCCAGCGAAGCTGATGT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AAAGCCAGCGACGCTGATGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACL44494 standard; DNA; 21 BP
 19-MAY-2004; 2004WO-US015645.
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                        20-MAY-2003; 2003US-0471729P
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                                                                                                                                                                                                                                                                                                                                                                                                                                          90.08;
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                                                                   Be X, Wei L, Slonim DK,
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                                                                                          WPI; 2005-075568/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                    treating cancer.
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                                            (AMHP ) WYBTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The present invention relates to a novel pharmaceutical composition
comprising: (a) an agent capable of modulating an expression level or
protein activity of a cancer-related transmembrane protein (GRTP) or gene
an antibody specific for a CRTP, or a T cell activated by a CRTP; and
(b) a carrier. The pharmaceutical composition may also comprise a
polymucleotide capable of inhibiting or decreasing the expression of the
CRTP by RNA interference or an antisense mechanism. The CRTPs of the
invention are selected from ABC4, C20orfio3, CACNAID, CDH6, CST, ENPP3,
FLJ1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
pharmaceutical composition is useful for treating cancer, liver cancer, kidney
cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
cancer, stomach cancer, and esophageal cancer. The present sequence is a
target oligonucleotide from one such CRTP for which short interfering
CRNAB (SIRNA) were produced. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
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Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                             Claim 3, SEQ ID NO 5566, 113pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                treating cancer.
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Matches
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The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein dethvity of a cancer-related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polymucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABC4, C20orf103, CACNAID, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, kidney cancer, stomach cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, prostate cancer. The present sequence is a CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
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                                                                                                                                                                                                                                                                                                                              21.8%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 23;
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Les 18; Conservative
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The present invention relates to a novel pharmaceutical composition

comprising: (a) an agent capable of modulating an expression level or

protein activity of a cancer-related transmembrane protein (CRTP) or gene
; an antibody specific for a CRTP, or a T cell activated by a CRTP; and

(b) a carrier. The pharmaceutical composition may also comprise a

polynucleotide capable of inhibiting or decreasing the expression of the

CRTP by RNA interference or an antisense mechanism. The CRTPS of the

creation are selected from ABCC4, C20orfulo3, CACNALD, CDR6, CST, ENPP3,

FLJ1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The

cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney

cancer, lung cancer, and scophageal cancer. The present sequence is a

target oligonucleotide from one such CRTP for which short interfering

target oligonucleotide from one such CRTP for which short interfering

target climate directly from WIPO at

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               cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
                                                                                                                                                                                                                     Gaps
pharmaceutical composition is useful for treating cancer, e.g. colon
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                                                                                                                                                                                 Score 16.4; DB 1; Length 21; Pred. No. 27;
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                                                                                                                                           Sequence 21 BP; 4 A; 5 C; 7 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDH6 target oligonucleotide, SEQ ID 5569.
                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                 21.3%;
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                                                                                                                                                                                                  Similarity
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Best Local 8
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Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (GFTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orfil03, CACNAID, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The

Cytostatic, Gene therapy, Vaccine, RNA Interference, cancer; 88; short interfering RNA; gene silencing.

19-MAY-2004; 2004WO-US015645. 20-MAY-2003; 2003US-0471729P.

(AMHP ) WYETH.

WO2005001092-A2.

Synthetic.

36-JAN-2005

CDH6 siRNA sense sequence, SEQ ID 6071.

(first entry)

24-MAR-2005

ACL44999;

ACL44999 standard; RNA; 21 BP.

ACL44999 ID ACL4

Wed Apr 19 16:15:55 2006

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The present invention relates to a novel pharmaceutical composition comportsing: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (RTP) or gene; an antibody specific for a GTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polymucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, CPLAI1856, GPR54, HAVCH1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a cancer, interfering RNAs GIRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but
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   Length 21;
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   DB 1;
Score 16.4; DE
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDH6 siRNA antisense sequence, SEQ ID 5571.
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21.3%;
94.4%;
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                                                                                                                         51 AGCCAGCGAAGCTGATGT
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                            15 Similarity 94.4
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Query Match
Best Local
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ACL4499/c
ID ACL4499/c
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The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (CRTP) or gene; an antibody specific for a CRTP, or a T cell activated by a CRTP; and (b) a carrier. The pharmaceutical composition may also comprise a polynucleotide capable of inhibiting or decreasing the expression of the CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, CRTP by RNA interference or an antisense mechanism. The CRTPs of the invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3, CTL1856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a cancer interfering RNBs (siRNA) oligonucleotide. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition comprising an agent capable of modulating expression level or protein activity of a gene, e.g. ABCC4, or a T ce activated by the polypeptide or antibody, and a carrier, useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 5 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 6071; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                    Wei L, Slonim DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-075568/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating cancer.
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AAT48824/C
1D AAT4888
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68

20 AGCCAGCGACGCTGATGT 3

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AGCCAGCGAAGCTGATGT

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The sequences given in AAT48821-34 are primers which were used to amplify regions of the type II non-pancreatic phospholipase A2 (PLA2s) gene at which mutations occur. These primers amplify regions upstream of the first exon and exon one, around the microsatellite, and exons 2, 3, 4 and 5 and the surrounding sequences. These primers may be used in the method of the invention for identifying an individual at an elevated risk of colon cancer. The method comprises: (a) isolating genetic material from a tissue or body fluid sample from the individual; and (b) detecting a plaze gene mutation which is indicative of the individual is at an elevated risk of colon cancer; or (b') detecting the absence of PLA2s protein or PLA2s enzyme activity in an isolated protein sample which is indicative of the individual having an elevated risk of colon cancer. The method allows individual having an elevated risk of colon cancer. The mutation to be identified. In the treatment of colon cancer, the patient is administered a recombinant vector incorporated within a non-toxic
                                         Polymerase chain reaction; PCR; amplify; primer; PLA2s; mutation; APC; type II non-pancreatic phospholipase A2; microsatellite; colon cancer; adenomatous polyposis coli; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying an individual at an elevated risk of colon cancer - by detecting mutation(s) in PLA2s gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enteric microorganism which expresses and secretes PLA2s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                              Chepenik KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 16; 78pp; English.
                                                                                                                                                                                                                                                                                                                                     (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                              95US-00484359.
                                                                                                                                                                                                                                                     96WO-US009009.
                                                                                                                                                                                                                                                                                                                                                                              Siracusa LD,
  PLA2s exon 1 primer, AB4
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                                                                                                                                                                    WO9641003-A1
                                                                                                                                                                                                                                                     06-JUN-1996;
                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                              Buchberg AM,
                                                                                                                                                                                                           19-DEC-1996.
                                                                                                                           Synthetic.
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20.8%; Score 16; DB 1; Length 20; 100.0%; Pred. No. 29; o; Indels ive 0; Mismatches 0; Indels
                                16; Conservative
 Query Match
Best Local Similarity
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77 crearcrercase s CTGATGTCCTGTCAAG 20 62 셤 à

ADZ97584 standard; DNA; 21 BP (first entry) 14-JUL-2005 ADZ97584; RESULT 20 

Canine SNP detection, forward PCR primer SEQ ID No:181.

animal breeding; genetic marker; SNP detection; allelic variation; infection; diabetes; hypertension; atherosclerosis; autoimmune disease; renal disease; neurological disease; PCR; primer; ss.

Canidae.

WO2005040350-A2

06-MAY-2005

25-OCT-2004; 2004WO-US035231.

24-OCT-2003; 2003US-0514180P 08-OCT-2004; 2004US-0617383P

(MMIG-) MMI GENOMICS INC.

Fantin D; Bates S, Denise S, Hutton M, Rosenfeld D, Kerr R,

WPI; 2005-333502/34.

Identifying animal genetic marker that influences trait for determining parentage or to infer breed/line in e.g. canines involves analyzing markers of genome-wide genetic marker map for association with genetic

Claim 44; SEQ ID NO 181; 145pp; English.

trait.

The invention relates to a method of identifying a companion animal companion arimal genetic marker that infiltences a phenotype or trait comprising analyzing companion animal genetic marker that infiltences the trait. Also described are: (1) a high companion animal genetic marker that infiltences the trait. Also described are: (1) a high companion animal system for setting the motion of a secociation animal system for determining the nucleotide accorrances at a series of companion animal system for setting system for determining the nucleotide accorrance of a series of companion animal system, and described are: (1) a high manner of companion animal system for setting system for determining the nucleotide contracts of companion animal system, and system for applying a liquid to the series of oligonucleotide to a polymucleotide sociation of sectises of companion animal system, and system for applying a liquid to the series of oligonucleotide to a polymucleotide sociation of sectises of companion animal system, and oligonucleotide to a polymucleotide sociation of sectises of companion animal system, and oligonucleotide occurrence of the system of oligonucleotide occurrence of the system of oligonucleotide probe and/or primaryprimary system of the most 3 position of mucleotide occurrence of a least one canne system of incleotide occurrence of a series of complement in the most 3 position of mucleotide occurrence of a least one system of complement in the most 3 position of mucleotide sociations of a complement in the most 3 position of mucleotide sociations and animal system of the s

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cc second primer selected from SEQ ID Nos 204-305 in the method of the invention. The method is useful for identifying a companion animal companion. The method is useful for identifying a companion animal comparation are to infer breed/line of a canine test subject, for identifying/inferring a genetic trait (preferably resistant to disease or infection), susceptibility to infection, regulation of immune status and response to antigens, previous exposure to infection or parasites, captibility to infection, the conformance status and response to antigens, previous exposure to infection or parasites, companion animal (preferably doss, cats, fish, reptiles, brids, horses, autoimmune disorders, kidney disease and neurological disease in companion animal (preferably doss, cats, fish, reptiles, birds, horses, captiles, hamsters, garbils, mice or rats, especially dos). The methods/eystems help for managing, selecting and breeding companion animals, maximizing individual potential performance and health, allowing predictive (predisposition) diagnostics, nutritional theraples and collect, record and store data by individual animal identification so that it is usable to improve future animals as applied to companion animals, companion animal, to animal to manage, sort, traits such as energy metabolism, aging and breed-specific traits to companion animal, to and improve the genetics of a companion animal, to an energy metabolism, aging and breed-specific taits of an dimprove the genetics of a companion animal, to manage, sort, and improve the genetics of a companion animal or offspring, and to diagnose a health condition of a companion animal or offspring, and to diagnose a health condition of a companion animal or offspring, and to diagnose correct trait, to track a companion animal or offspring, and to diagnose a health condition of a companion summal. This sequence represents a per expresents a per correction of canine some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 1; Length 21;
Pred. No. 33;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDH6 siRNA sense sequence, SEQ ID 5570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Howes SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 TGAGAGGTAAAGAGCCAGC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGTGGTAAATAGCCAGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACL44498 standard; RNA; 21 BP
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89.5%;
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The present invention relates to a novel pharmaceutical composition comprising: (a) an agent capable of modulating an expression level or protein activity of a cancer-related transmembrane protein (GRTP) or gene; an antibody specific for a GRTP, or a T cell activated by a CRTP; and (D) a carrier. The pharmaceutical composition may also comprise a cRTP; and cRTP by RNA interference or an antibense mechanism. The expression of the cRTP by RNA interference or an antibense mechanism. The CRTPs of the invention are selected from ABC4, C20orfi03, CACNAID, CDH6, CST, ENPP3, FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The pharmaceutical composition is useful for treating cancer, e.g. colon cancer, stomach cancer, prostate cancer, liver cancer, kidney cancer, stomach cancer, and esophageal cancer. The present sequence is a CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence cate for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new human KIAA0172 gene. The KIAA0172 gene and polypeptide are useful for detection and treatment of cancer. The present sequence represents KIAA0172 associated primer.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 3 A; 5 C; 8 G; 0 T; 5 U; 0 Other;
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(INFO-) INFO GENES CO LID.
(KAZU-) ZH KAZUSA DNA KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 22 BP; 5 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      20.0%; Score 15.4; F
76.5%; Pred. No. 38;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; KIAA0172; cancer; ss; PCR; primer.
Claim 3; SEQ ID NO 5570; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCAGCGACGCUGAUGU 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 GCCAGCGAAGCTGATGT
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1es 13; Conservative
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Matches 16, Conserv
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Matches
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(first entry)

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The present invention relates to an antisense compound targeted to a mucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to disher path pain, post-herpetic neuralgia, chronic pain, lower back pain, pain from burns, migraine headache, cluster headache, mid-to-moderate puin from burns, migraine headache, cluster headache, mid-to-moderate but not limited to neonatal or infantile epilepsy, or ataxia. The present sequence represents a chimeric phosphorothioate oligonuclectife with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                          Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; 8s.
                                                                                                  Chimeric phosphorothioate oligonucleotide to target Navl.3 #208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 208; 417pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2002; 2002US-0403416P.
                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2003; 2003WO-US025465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-203785/19.
                                                                                                                                                                                                                                                                                                         WO2004016754-A2
                                               20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                           26-FEB-2004
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                                                                                                                                                                                                                                                         Synthetic.
ADK72874;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Navl.3, where the antisense compound specifically hybridizes with and inhibits the expression of Navl.3. The compound and composition are useful for treating a disease or condition associated with Navl.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuropathy, arthritic pain, lower back pain, diabetic neuropathy, triggminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothicate oligonuclectide with 2 MOB wings and a deoxy gap. Used during the antisense inhibition of human Navl.3 expression, the oligonuclectides are designed to target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                         Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss.
                                                                                                                                                                                                                                                                                                                                                           Chimeric phosphorothicate oligonuclectide to target Nav1.3 #188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.7%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 39; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            different regions of the human Nav1.3 RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 188; 417pp; English.
                          16
                                                                          AGCTGATGGCCTGTCAA 18
                                                                                                                                                                                                    ADK72854 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2003; 2003WO-US025465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2002; 2002US-0403416P
                          60 AGCTGATGTCCTGTCAA
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-203785/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004016754-A2.
                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                      ADK72854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
2'MOB wings and a deoxy gap. Used during the antisense inhibition of human Navl.3 expression, the oligonucleotides are designed to target different regions of the human Navl.3 RNA.
                                                                                                                                            Gaps
                                                                                                                                          ö
                                                                                                        19.7%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 39;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Human chromosome 1p36-35 PCR primer SEQ ID NO:1533.
                                                                        Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                          0; Mismatches
                                                                                                                                                                             35 CCTCTGAGAGGTAAAGAGCC 54
                                                                                                                                                                                                               ccrcregaaggcaaagagcc 1
                                                                                                                                                                                                                                                                                                    ABL44489 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                        11-APR-2002 (first entry)
                                                                                                                          Best Local Similarity 85.0 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                        ABL44489;
                                                                                                            Query Match
                                                                                                                                                                                                                                                                  RESULT 25
ABL44489/c
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Gaps

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TCCTCTGAGAGGTAAAGAGC 53

Conservative

Local Similarity

TCCTCTGGAAGGCAAAGAGC 1

20

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2874/c ADK72874 standard; DNA; 20 BP

ADK72874/ ID ADK7 RESULT

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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in mittinell plates numbered for discrimination are mixed in each of the multiwell plates to be primer designed based on the chromosome marker multiwell plates; (b) a primer designed based on the chromosome marker compared to corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order compared to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. to array the multiwell compared in the multiwell plates of the specified and lateral directions; (f) the mixed clones are cultured and the cresultant cultures are maxed respectively in each wells of longitudinal consultant cultures are amplified by using the above primer; (g) signals and detected from the amplified by using the above primer; (g) signals reconstituted as the positions on the chromosome and arrayed. The cremestive sequence for human chromosome alones are present compared for human chromosome 21q22.1, which are separed for use in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Drosophila suppressor; human hedgehog-patched pathway; HH-PTC; sonic hedgehog-patched pathway; SHH-PTC; intracellular signal; split hand; split foot malformation type 3; SHHW3; wound healing; neurodegenerative disease; testicular; cancer; gene therapy; cytostatic; neuroprotective; rapid amplification of cDNA end; RACE; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RACE PCR primer #1, used for cloning human SU(FU) homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.2%; Score 14.8; DB 1; Length 20; ilarity 88.9%; Pred. No. 44; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           Claim 4; Page 35; 528pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAAGAGCCAGCAAAGCT 1
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                                                                                                                            10-MAR-2000; 2000JP-00066716.
                                                                                        12-MAR-2001; 2001JP-00068285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAAGAGCCAGCGAAGCT
                                                                                                                                                             (RIKA ) RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD35822 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                       Arraying genome clones.
                                                                                                                                                                                                                   WPI; 2002-144136/19
                                                                                                                                                                              (GENO-) GENOTEX YG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 16; Conserv
                  JP2001321190-A.
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                                                    20-NOV-2001.
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Matches
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The invention relates to proteins, polypeptides and nucleotides related to the human homologue of the Drosophila suppressor of fused gene, which is involved in the transduction of signals in the human hedgehog-patched (HH-PTC) pathway. Protein molecule capable of eliciting an intracellular signal in the HH-PTC pathway, its antibodies and pharmaceutical compositions comprising them can be used as medicaments for the treatment and/or prevention of split hand/split foot malformation type 3 (SHRM3). The polymucleotides and polypeptides of the invention can be used to gain an understanding of a signalling pathway that is central to normal development and often disrupted in disease. This knowledge will be value for therapeutic strategies involving modification of sonic hedgehog-tissue/wound healing, neurodegenerative diseases, testicular function and cancer. The polymucleotides of the invention may also be used in gene therapy methods. The present sequence is a rapid amplification of CDNA ends (RACE) PCR primer used for cloning human SU(FU) homologue. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic, neuroprotective, suppressor of fused; SUFU; signal transduction; patched receptor; hedgehog ligand; hedgehog-patched pathyway; HH-PTC pathway; Split hand/Split foot Malformation Type 3; SHFM3; sonic hedgehog-patched; SHH-PTC signal pathway; tissue healing; wound healing; energenerative disease; testicular function; cancer; gene therapy; human; SUFUH; PCR; primer; 88.
                                                                                                                                                                                                 Human homolog of the Drosophila suppressor of fused gene useful in the treatment of Split hand/Split foot Malformation Type 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.2%; Score 14.8; DB 1; Length 21; 88.9%; Pred. No. 47; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2, Indels
                                                                                                                              Grimm T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human suppressor of fused (SUFUH) primer segid 3.
                                                                                                                          loftgard R, Zaphiropoulos PG, Kogerman P,
                                                                                        (KARO-) KAROLINSKA INNOVATIONS AB
                                                                                                                                                                                                                                                         Example; Page 67; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 caaccrearcracrecca 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADT92489 standard; DNA; 21 BP
                                  97SE-00004788.
98SE-00002293.
98WO-SE002383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2000; 2000US-00581831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97SB-00004788
98SB-00002293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GAAGCTGATGTCCTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 88.5 es 16, Conservative
                                                                                                                                                               WPI; 1999-405160/34.
 18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6448020-B1.
                                  19-DEC-1997;
                                                     26-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADT92489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADT92489
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The invention describes novel human homologues to molecules associated with the Drosophila suppressor of fused (SUFU) gene. These molecules are with the Drosophila suppressor of fused (SUFU) gene. These molecules are interaction between the patched receptor and any one of the hedgehog control of the human hedgehog patched (HH-PPC) pathway and intracellular signal in the human hedgehog-patched (HH-PPC) pathway and exhibiting a substantial similarity (sepecially about 80%), the amino acid sequence is not given in the specification; an isolated human DNA sequence (II) capable of involvement in eliciting an intracellular signal in the HH-PPC pathway, the nuclectide sequence (3); thracellular signal in the HH-PPC pathway, the nuclectide sequence (3); and cyression cassette comprising (II) or the DNA sequence (3); a cell comprising the expression cassette of (5); an antibody that binds (1) or their variants, a vector comprising (II) or the DNA sequence (3); a cell comprising the expression cassette of (5); an antibody that binds (1); a recombinant cell expressing that binds (2); a recombinant cell expressing the antibody of (7); a kit for the detection of a human suppressor of fused gene, comprising a nucleic acid sequence capable of hybridising specifically with (II); and and some capable of hybridising specifically with (II); and nucleic acid sequence capable of hybridising specifically with (II); and and split for Malformation Type 3 (SHFM3). The polymucleotides and polympetides can be used to gain an understanding of a signaling pathway companies and pharmaceutical compositions comprising a modification of sonic hedgehog-patched (SHH-PTC) signaling pathway. The knowledge will be value for therapatch extractive diseases, testicular function and cancer. The polymucleotide may also be used in gene therapy methods. This sequence represents a primer used to isolate the sequence represents a primer used to isolate the sequence of fused (SUFWH).
                                                                                                                                                                                                                   fused gene useful in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                 Human homolog of the Drosophila suppressor of fused ger
treatment of Split hand/Split foot Malformation Type 3.
                                                                                                                                Grimm T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
                                                                                                                              Toftgard R, Zaphiropoulos PG, Kogerman P,
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0; Mismatches
                                                                                                                                                                                                                                                                                  Example; SEQ ID NO 3; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MRCK2 siRNA sequence SeqID14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 GAAGCTGATGTCCTGTCA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADS93548 standard; RNA; 21 BP
18-DEC-1998; 98WO-SE002383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                      (TOFT/) TOFTGARD R.
(ZAPH/) ZAPHIROPOULOS P G.
(KOGE/) KOGERMAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                        WPI; 1999-405160/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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muscular-Gen; osteopathic; cardiovascular-Gen; immunosuppressive; cerebroprotective; vasotropic; anticonvulsant; anti-HIV; MRCKZ-modulator; gene therapy; inflammation; cancer; arteriosclerosis; psoriasis; asthma; Parkinson's disease; rheumatoid arthritis; spinal cord injury; muscle condition; osteoporosis; graft versus host disease; cardiovascular disorder; autoimmune disorder; retinal detachment; stroke; epilepsy; ischaemia; reperfusion; breast cancer; ovarian cancer; glioblastoma; non-Hodgkin's lymphoma; colorectal cancer; ovarian on-emall cell lung cancer; brain cancer; Kaposi's sarcoma; pancreatic cancer; liver cancer; tumour; siRNA; short interfering RNA; New isolated polypeptide, useful for preventing or treating a myotonic dystrophy kinase-related Cdc42 binding kinase 2 (MRCK2)-related disease e.g., inflammation, cancer, arteriosclerosis, psoriasis, and Parkinson's This invention relates to a novel isolated human protein kinase, MCRK2 Disclosure; SEQ ID NO 14; 242pp; English. 07-OCT-2003; 2003WO-US031591 07-OCT-2002; 2002US-0416257P WPI; 2004-340908/31. WO2004033638-A2 (LIUW/) LIU W. (WULL/) WU L. Wu L; Homo sapiens. 22-APR-2004. human; ss. e.g., inf disease. Liu W, 

This invention relates to a novel isolated Animan profesh Kinase, WCKKC.

This invention relates to a novel isolated Animan profesh Kinase, with sequence shows homology to rat myotconic dystrophy kinase-related cod-12 binding kinase 2 (WECK2). The gene encoding the novel kinase is localised to human in locus 142 of human chromesome. The novel protein will be profesh may functional/structural domains that include a kinase domain, a pichein may function as a downstream effector of Cdc42 in command. The invention may be useful for the production of cytostatic, antinflammatory, antiarteriosclerotic, ophthalmological, antipsoriatic, antishfammatory, antiarteriosclerotic, ophthalmological, antipsoriatic, antishfumatic, antiarteriosclerotic, or antirheumatic, antipsoriated, antiaschmatic, antiartheumatic, antiartheumatic, antiartheumatic, cantingsoriated, antiartheumatic, and any perventing or treating an myotonic dystrophy kinase-related cdc42 binding kinase 2 (WECK2) -Inhibitors or MRCK2-Modulator. In subject such as inflammation, cancer, arteriosclerosis, psoriasis, as subject such as inflammation, cancer, arteriosclerosis, psoriasis, cardiovascular disorders, autoimume disorders, retinal detachment, stroke, epilepsy, isobaematic, fraperfusion, brasst cancer, our-anditions, cancer, brain cancer, Kaposis, grarcoma, pancer, brain cancer, Kaposis, sarcoma, pancer, and other tumours. The MRCK2 and MRCK2 gene are useful as models (for the development of human therapeutic targets, and in the calculation of therapeutic proteins, and serve as targets for the identification of therapeutic proteins. The MRCK2 and MRCK2 gene

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Gaps

Sequence 21 BP; 5 A; 4 C; 5 G; 0 T; 7 U; 0 Other;

human protein kinase; MCRK2; myotonic dystrophy kinase-related Cdc42 binding kinase 2; 1q42; chromosome 1; pkinase C domain; DAG-PB; CNH domain; cytoskeleton reorganisation; cytostatic; antiinflammatory; antiarteriosclerotic; opthalmological; antipsoriatic; antiasthmatic; antiparkinsonian; antirheumatic; antiarthritic; neuroprotective;

DB 1; Length 21; 19.2%; Score 14.8; I 88.9%; Pred. No. 47; Best Local Similarity Query Match

hGDMLP-1; heart; heart disease;

Human GDMLP-1 17-mer scanning SRQ ID NO:5 sequence SEQ ID NO:10026.

(first entry)

29-MAY-2002

ABN10034;

Human, genome-derived myosin-like protein 1, GDMLP-1, muscle, myosin, chromosome 22, gene therapy, vaccine, skeletal muscle disorder, amplicon, screening; ss.

ABN10034 standard; DNA; 17 BP

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The present invention relates to a novel pharmaceutical composition

comprising: (a) an agent capable of modulating an expression level or

protein activity of a cancer-related transmembrane protein (GRPP) or gene

an antibody specific for a CRPP, or a T cell activated by a CRTP; and

(b) a carrier. The pharmaceutical composition may also comprise a

polymucleotide capable of inhibiting or decreasing the expression of the

CRTP by RNA interference or an antisense mechanism. The CRTPs of the

invention are selected from ABCC4, C20orf103, CACNAID, CDH6, CST, ENPP3,

PLAIDS6, GRRF4, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The

pharmaceutical composition is useful for treating cancer, e.g. colon

cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney

cancer, stomach cancer, and esophageal cancer. The present sequence is a

CRTP short interfering RNAS (SIRNA) oligomucleotide. Note: The sequence

data for this patent did not form part of the printed specification, but

cancer, interfering and compare of the printed specification, but

cancer, interfering and compare of the printed specification, but

cancer, interfering and compare of the printed specification, but

cancer, interfering and compare of the printed specification, but

cancer, interfering and compare of the printed specification, but
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pharmaceutical composition comprising an agent capable of modulating an expression level or protein activity of a gene, e.g. ABCC4, or a T cell activated by the polypeptide or antibody, and a carrier, useful for
      Gaps
                                                                                                                                                                                                                                                                                                                                               Cytostatic, Gene therapy, Vaccine, RNA Interference, cancer, 88; short interfering RNA, gene silencing.
    ö
  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 6 A; 6 C; 5 G; 0 T; 4 U; 0 Other;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Etp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 5564; 113pp; English
                                                                                                                                                                                                                                                                                                         CDH6 siRNA sense sequence, SEQ ID 5564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Howes SH;
  ö
                                          41
                                                                 21 AAGTCTAGAGTCCTCTGA 4
                                                                                                                                                                                    뎚
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-2004; 2004WO-US015645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-2003; 2003US-0471729P
                                          24 AACTCTGGAGTCCTCTGA
                                                                                                                                                                                  ACL44492 standard; RNA; 21
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Be X, Wei L, Slonim DK,
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-075568/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2005001092-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMHP ) WYETH.
                                                                                                                                                                                                                                                                   24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JAN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                        ACL44492;
Matches
                                                                                                                                     RESULT 28
ACL44492
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 mucleic acids can be used as probes to detect, characterise and quantify concleid acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 provided initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically proteins, as specifically recognise hGDMLP-1 proteins, as specific biomolecule and/or amount specifically of hGDMLP-1 may be used for diagnosing a charageutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. at ftp.wipo.int/pub/published_pct_sequence
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Gaps

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2; Indels

19.2%; Score 14.8; DB 1; Length 21;

Pred. No. 47; 2; Mismatches

77.8%;

14; Conservative

Matches

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RESULT 30

ABN10034

Local Similarity

Query Match

49 AGAGCCAGCGAAGCTGAT 66 AAAGCCAGCGACGCUGAU 20

New polypeptide, for raiging antibodies that recognize hGDMLP-1 proteins,

Shannon ME;

Chen W,

Rank DR,

Gu Y, Ji Y, Penn SG, Hanzel DK,

(AEOM-) AEOMICA INC

WPI; 2002-179446/23.

2001WO-US000668. 2001WO-US000669. 2001WO-US000670.

2001US-0266860P

05-FEB-2001;

10-JAN-2001

2001WO-US000667

30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

2000US-0234687P 2000US-0236359P

2000GB-00024263

2001WO-US0006

25-MAY-2001; 2001WO-US016981

26-MAY-2000;

21-SEP-2000

WO200192524-A2.

06-DEC-2001

Homo sapiens

2001WO-US000662 2001WO-US000663 2001WO-US000664 2001WO-US000665

30-JAN-2001;

30-JAN-2001;

04-OCT-2000

30-JAN-2001;

or as specific blomolecule capture probes for surface-enhanced laser descrption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 10026; 214pp; English.

Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   desorption ionization, comprises human myosin-like protein hGDMLP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shannon ME
                                                                  ö
18.7%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 42;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 10027; 214pp; English
                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000; 2000GB-00024263.
30-JAN-2001; 2001WO-US000661.
30-JAN-2001; 2001WO-US000662.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000666.
                                                                                                                                                                                                                                                                                                                                                       ABN10035 standard; DNA; 17 BP
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2000GB-00024263.
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30-JAN-2001; 2001WO-US000670.
05-FEB-2001; 2001US-0266860P.
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                             93.88;
                                                                                                                                27 TCTGGAGTCCTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                              15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AEOM-) AEOMICA INC.
                                 Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200192524-A2
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                      ABN10035;
   Query Match
                                                                                                                                                                                                                                                                                         ABN110035

ID ABN110035

ID ABN110035

ABN11
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polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived
                                                                                                                                                                                                                                                                                                                                                                       Human; 88; probe; myosin-like protein-1; hGDMLP-1;
hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shannon ME;
                                                                                                                                                                ö
                                                                                                                                     18.7%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 42;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                              Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ď
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank
                                                                                                                                                                                                                                                                                                                                                   Human GDMLP-1 probe SEQ ID NO:10027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US000665.
2001WO-US000667.
2001WO-US000667.
2001WO-US000669.
2001WO-US000670.
2001WC-US000670.
                                                                                                                                                                                                                                                                           ACN73125 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US000663.
2001WO-US000664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-US000661
2001WO-US000662
                                                                                                                                                                                        27 TCTGGAGTCCTCTGAG
                                                                                                                                                                                                                                                                                                                           02-DEC-2004 (first entry)
                                                                                                                                                                15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ji Y, Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHANNON M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENN S G.
HANZEL D K.
RANK D.
CHEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPI; 2004-533378/51.
                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      hGDMLP-1 agonist
skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004137589-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001;
05-FEB-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RANK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PENN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HANZ/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gu Y,
                                                                                                                                                                Matches
                                                                                                                                                                                                                                                 RESULT 32
     88888888888888
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5981732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COWBERT LAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                      function.
                                                                                                                                                                                                                                                                                                                                                                                                  AAZ31818;
                                                                                                                                                                                                                                                                                                                                                          RESULT 34
AAZ31818/c
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                                                      (S1) of myosin-like protein-1 (hoDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 958 deviation from (S1) which are conservative substitutions, and 658 identity to (S1). A polypeptide of the invention acts as a sgonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103
myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                               comprising a sequence
                                                                                                                                                                                                                                                                                                                                                                              Human; ss; probe; myosin-like protein-1; hGDMLP-1;
hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                           ö
                                                                                                                                                                                    18.7%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 42; ive 0; Mismatches 1; Indels
                                                                                                                                                                   Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
                                               The invention relates to a novel polypeptide (I)
                          Disclosure, SEQ ID NO 10027; Opp; English
                                                                                                                                                                                                                                                                                                                                                            Human GDMLP-1 probe SEQ ID NO:10026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000; 2000GB-00024263.
30-JAN-2001; 2001WO-US000661.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000670.
                                                                                                                                                                                                                              27 TCTGGAGTCCTCTGAG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0236359P
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2001US-00866108
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                                                                                                                                                                                                                                                                                                  ACN73124 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         hGDMLP-1 agonist hGDMLP a
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENN S G.
HANZEL D K.
RANK D.
CHEN W.
                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004137589-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       원
11 Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SBP-2000;
                                                                                                                                                                                                                                                                                                                                        02-DBC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2004.
                                                                                                                                                                                                                                                                                                                    ACN73124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PENN/)
(HANZ/)
(RANK/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GUYY/)
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                               RESULT 33
                                                                                                                                                                                                                                                                                           ACN73124
셤
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The invention relates to a novel polypeptide (I) comprising a sequence (SI) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a tragment of at least 8 amino acids fully (SI), 95% deviation from (SI) which are conservative substitutions, and antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of HGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                             Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents an antisense inhibitor of the invention, and inhibits the expression of the human G-alpha-13 protein. The antisense compounds of the invention are of 8 to 30 nucleobases in length, that inhibits the expression of the human G-alpha-13. The antisense compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-alpha-13; human; inhibitor; cancer; antisense compound; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                    Shannon MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.7%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 42; tive 0; Mismatches 1; Indels
                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G-alpha-13 antisense inhibitor ISIS# 20767.
                                                                    Rank D,
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 10026; Opp; English
                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11, Col 39, 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00205860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ31818 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 TCTGGAGTCCTCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.7
Best Local Similarity 93.8
Matches 15, Conservative
                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
(SHAN/) SHANNON M B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-633376/54.
                                                                                                                                            WPI; 2004-533378/51.
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is useful for treating an animal, particularly humans, having or being prone to a disease or condition associated with the expression of G-alpha -13, such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compound targeted to a nucleic acid molecule encoding bava.13, useful for useful for treating a disease or condition associated with Navl.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric phosphorothioate oligonucleotide to target Navl.3 #1994.
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                                                                                                                        DB 1; Length 18;
                                                                                                                                                          1; Indels
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                                                                                    Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                      ; Score 14.4; DE; Pred. No. 45; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 1994; 417pp; English
                                                                                                                                                                                                                                                                                                                        ADK74660 standard; DNA; 20 BP.
                                                                                                                    Match 18.7%;
Local Similarity 93.8%;
He 15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2003; 2003WO-US025465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                              ADK74660;
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                      RESULT 35
ADK74660/c
                                                                                                                                                          Matches
               SKSSS
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The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, lower back pain, pean from burns, migraine headache, cluster headache, mild-to-moderate bain from burns, migraine headache, cluster headache, mild-to-moderate but not limited to neonatal or infantile epilepsy, or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2.7ME wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                                                                                                           Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                               Chimeric phosphorothicate oligonucleotide to target Navl.3 #565
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Pred. No. 55;
0; Mismatches 3; Indels
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54
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ID ADP12043 standard; DNA; 20 BP.
XX
AC ADP12043;
36 CTCTGAGAGGTAAAGAGCC
                    20 CTCTGGAAGGCAAAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2003; 2003WO-US025465.
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ADK73231 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-203785/19.
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                                                                                                                                                                               20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roberds SL;
                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                ADK73231;
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Gaps

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Query Match 18.4%; Score 14.2; DB 1; Length 20; Best Local Similarity 84.2%; Pred. No. 55; Matches 16; Conservative 0; Mismatches 3; Indels

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The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, e.g. neathous cell transplant rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIVAIDS or viral, bacterial or fungal infection. The present sequence represents a primer for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                         transplant rejection; immune system; rheumatoid arthritis; lupus;
inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.
                                                                                                                                                                                                                                                                                                                                                                                                           Ly N, Prentice J, Morris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 20;
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                                                      Set 2 right PCR primer for marker probe #149.
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                                                                                                                                                                                                                                                                                                                                                                                                           Woodward R,
                                                                                                                                                                                                                                                                                                                                                                     (EXPR-) EXPRESSION DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                       24-APR-2003; 2003WO-US012946.
                                                                                                                                                                                                                                                                                                            24-APR-2002; 2002US-00131831.
20-DBC-2002; 2002US-00325899.
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           Wohlgemuth J, Pry K,
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Best Local Similarity
                                                                                                                                                                                          WO2004042346-A2
                                                                                                                                                          Homo sapiens.
                  12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                Rosenberg S;
                                                                                                                                                                                                                                   21-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the genes.
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New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 10025; 214pp; English

Shannon MB;

Chen W,

Hanzel DK, Rank DR,

Ji Y, Penn SG,

Gu Y,

WPI; 2002-179446/23.

(AEOM-) AEOMICA INC.

2000US-0236359P

2000GB-00024263 2001WO-US000661

04-OCT-2000; 21-SEP-2000 26-MAY-2000 27-SEP-2000

25-MAY-2001; 2001WO-US016981

WO200192524-A2. Homo sapiens.

06-DEC-2001

2001WO-US000663 2001WO-US000663 2001WO-US000664

30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

2001WO-US000665. 2001WO-US000666. 2001WO-US000667.

30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

2001WO-US000669. 2001WO-US000669. 2001WO-US000670.

30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 05-PEB-2001;

2001US-0266860P

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polymucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 mucleic acids can be used as probes to detect, characterise and quantify chgMLP-1 nucleic acids in samples, as amplification substrates, to protein variants having desired phenotypuc improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific blomclecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in parients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production used the apprecase in disorders associated with the expression of hGDMLP-1, in particular heart of all sorders associated with the expression of hGDMLP-1, in particular heart can associated with the expression of the present invention. N.B. The sequence data for this patent did not form part of the printed captured that for this patent did not form part of the printed captured that for this patent did not form part of the printed captured the character of the present invention. The production will be concentrated the character of the printed captured the character of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ned in electronic format directly from WIPO
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18.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
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3; Indels

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16; Conservative

Matches

20

32 AGTCCTCTGAGAGGTAAAG

20 Acrecreceaeaeceaae 2

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ABN10033 standard; DNA; 17 BP

RESULT 38 ABN10033

Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10025.

(first entry)

29-MAY-2002

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ABN10033;

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ABN10032;

06-DEC-2001

Pred. No.

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Query Match
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Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

18.2%; Score 14; DB 1; Length 17;

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100.0%;
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                           27 TCTGGAGTCCTCTG
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HANZEL D K.
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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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25-MAY-2001;
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27-SEP-2000;
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(SHAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENN/
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                                                                                                                                                                                                                                               RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 mucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specifically and/or and/or amount specifically proteins, as specific biomolecule and/or amount specifically proteins, as specific biomolecule and/or amount specifically proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as theraputic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed content of the present invention. N. B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat figure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                          Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                       Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10024.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 10024; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000; 200059-0255595.
04-OCT-2000; 200058-00024263.
30-JAN-2001; 2001WO-US000662.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000669.
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2000US-0236359P.
2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456P
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                           Ношо варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel polypeptide (I) comprising a sequence (SI) of myosin-like protein-1 (MDMLP-I) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (SI), 95% deviation from (SI) which are conservative substitutions, and 65% identity to (SI). A polypeptide of the invention acts as a agonist antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or
                                                                                                                                                                                                   Human; 88; probe; myosin-like protein-l; hGDMLP-l;
hGDMLP-l agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
 Gaps
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 Indels
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Mismatches
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                                                                                                                                                                                 Human GDMLP-1 probe SEQ ID NO:10024.
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                                                                                                            ACN73122 standard; DNA; 17 BP.
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2001WO-US000665.
2001WO-US000666.
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2001MO-US000669.
2001MO-US000669.
2001MO-US000670.
2001US-O26680P.
2001US-00866108.
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2001WO-US000662
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preventing a disorder associated with decreased expression or activity hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                                                                                                                                                                                Human; 88; probe; myosin-like protein-l; hGDMLP-l;
hGDMLP-l agoniet hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
                                                                                                       Gaps
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                                 invention for scanning the sequence represented in ACN63103
                                                                             18.2%; Score 14; DB 1; Length 17; 100.0%; Pred. No. 49; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                        Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                              Human GDMLP-1 probe SEQ ID NO:10025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
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30-JAN-2001; 2001WO-US000661.
30-JAN-2001; 2001WO-US000662.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000669.
20-JAN-2001; 2001WO-US000670.
65-FRB-2001; 2001WS-USC6860P.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                         ACN73123 standard; DNA; 17
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                                                                                                    Conservative
                                                                                                                          TCTGGAGTCCTCTG
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                                                                          Query Match
Best Local Similarity
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HANZEL D K.
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CHEN W.
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                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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(PENN/)
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(CHEN/)
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Matches
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ID ACN7
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The invention relates to a novel polypeptide (I) comprising a sequence (SI) of myosin-like protein-1 (MDDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (SI), 95% deviation from (SI) which are conservative substitutions, and 65% identity to (SI). A polypeptide of the invention acts as a agonist antagonist of hODMLP-1, or as an inhibitor of hODMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human sodium-hydrogen exchanger like protein 1 (NHBLP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human
                                                                                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
NHBLP1; passive replacement therapy; vaccine; diagnosis.
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                                                                                                                                                                                                              invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                     DB 1; Length 17;
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                                                                                                                                                                                                                                                  Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                          18.2%; Score 14; DB 100.0%; Pred. No. 49; ive 0; Mismatches
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23-MAY-2001; 2001US-00864761.
21-DEC-2001; 2001US-0343331P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC04443 Standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                      TCTGGAGTCCTCTG 16
                                                                                                                                                                                                                                                                                                                                                                              27 TCTGGAGTCCTCTG 40
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                                                                                                                                                                                                                                                                                                               Local Similarity 100.
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ID ADC044
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Matches
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Pred. No.

93.3%;

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The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGP-R) is activated in an autocrime manner, inhibits the growth of these cells. The isolated in peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Rap-Gh-Glu-Glu-Lys (P2) Lys-Lew-Met-Ser-Tyr (P3) Phe-Phe-Phe-His-Pro-Val (P5) (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, percessarcoma, malanoma, machoma, neuroblastcoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (anglogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.
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diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide spanning the sequence of the human NHELP1 gene (ADC03514).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; canc carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
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                                                                                                                                                                     17.9%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 53; ive 0; Mismatches 2; Indel8
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                                                                                                       Sequence 17 BP; 2 A; 5 C; 3 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                     17 AATGAGCCAGCGAAGAT
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                                                                                                                                                                                                                                                   15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HAAL/) HAALAND P D.
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                                                                                                                                                                                                                  Local Similarity
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ID ADJ8

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17.4%; Score 13.4; DB 1; Length 15;

Query Match

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates to hGDMLP-1 protein variants abstrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP capture probes for surface-enhanced laser described in ionisation and/or amount specifically of hGDMLP proteins, as specific blomolecule capture probes for surface-enhanced laser description ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                            Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                    Gaps
                                                                                                                                                                                                                                                               Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shannon ME;
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                    Indels
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                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 10028; 214pp; English
   ed. No. 52;
Mismatches
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2001WO-US000662.
2001WO-US000663.
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2000US-0236359P.
2000GB-00024263.
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30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
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05-FEB-2001; 2001US-0266860P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2001; 2001WO-US016981
                                                    73
                                                                                   1 AAGCTGATGTCCTAT 15
                                                                                                                                                                  ABN10036 standard; DNA; 17
                                                                                                                                                                                                                                 (first entry)
                      14; Conservative
                                                    59 AAGCTGATGTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gu Y, Ji Y, Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-179446/23.
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              WO200192524-A2.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
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                                                                                                                                                                                                  ABN10036;
                                                                                                                                  RESULT 44
                                                                                                                                                     ABN10036
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ö disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; isolated nucleic acid, useful for treating viral diseases associated a tumors and cell degeneration, also related polypeptides, antibodies Gaps ö Tumour suppression related human fukutin oligo SEQ ID No 3657. antisense; sense; tumour; cell degeneration; cancer; Alzheimer schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds. DB 1; Length 17; 1; Indels Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other; Score 13.4; DE Pred. No. 61; 0; Mismatches Disclosure; Page 461; 720pp; French. Ξ Tuijnder Bb (MOLE-) MOLECULAR ENGINES LAB 17.4%; 17-SEP-2001; 2001FR-00011978. 17-SEP-2002; 2002WO-IB004208 42 crecaercerere 15 Deery Match
Best Local Similarity 93.35,
Best Local Similarity 93.45, 020/c ABT38020 standard; DNA; 17 (first entry) 28 CTGGAGTCCTCTGAG with tumors and cell de and transfected cells. relerman A, Amson R, WPI; 2003-313353/30. WO2003025175-A2 Homo sapiens 12-JUN-2003 27-MAR-2003. ABT38020; ABT38020/c
ID ABT38020/c
XX ABT38
XX AB RESULT 45 88888888888 셤 ठ

patient samples is useful for diagnosis and/or prognosis of these

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diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
NHBLP1; passive replacement therapy; vaccine; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Na/H exchanger-like protein 1 gene oligonucleotide #891
                                                                                                                                                                                                DB 1; Length 17;
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                                                                                                                                                                                                                                             Indels
                                                                                                                                                 Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                           Score 13.4; DI
Pred. No. 61;
0; Mismatches
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Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 931; 468pp; English.
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23-MAY-2001; 2001US-00864761.
21-DEC-2001; 2001US-0343331P.
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93.3%;
                                                                                                                                                                                                                                                                                        29 TGGAGTCCTCTGAGA 43
                                                                                                                                                                                                                                                                                                                      TGGAGTCTTCTGAGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC04444 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AEOM-) AEOMICA INC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid molecule which encodes a Na+/H+ exchanger like protein (NHELPI). The NHELPI nucleic acid molecule, NHELPI polypeptide, an antibody against the protein or its antigen-binding fragment is useful in therapy. The NHELPI nucleic acid molecule, NHELPI polypeptide and an agonist are particularly useful for manufacturing medicament for treating or preventing a disorder associated with decreased expression or activity of human NHELPI. The antibody or its antigen-binding fragment, and an antagonist, are useful for manufacturing a medicament for treating or preventing a disorder associated with increased expression or activity of human NHELPI. The NHELPI nucleic acid or protein is useful as passive replacement therapy, as a vaccine, or in diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide spanning the sequence of the human NHELPI gene (ADC03514).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human
 Gaps
                                                                                                                                                                                                                                                                                            88; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
NHBLP1; passive replacement therapy; vaccine; diagnosis.
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                                                                                                                                                                                                                                                             Human Na/H exchanger-like protein 1 gene oligonucleotide #892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.4; DB 1; Length 17;
Pred. No. 61;
0; Mismatches 1; Indels
 Indels
 1;
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Mismatches
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23-MAY-2001; 2001US-00864761.
21-DEC-2001; 2001US-0343331P.
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                                  47 AAAGAGCCAGCGAAG 61
                                                                                                                                                       ADC04445 standard; DNA; 17
                                                                  AATGAGCCAGCGAAG 2
                                                                                                                                                                                                                           (first entry)
14; Conservative
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                                                                                                                                                                                         ADC04445;
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 Matches
                                                                                                                        RESULT 47
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the conclectides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour cupression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or viral infections or diseases characterized by developmental.

Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can and/or prognosis of these diseases.
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                                                                                                                                               primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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                                                                                                                             antiviral; neuroprotective; nootropic; neuroleptic; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used to screen for their specific interactive molecules, ally useful for treating diseases associated with abnormal
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                                                                                        Tumour suppression/reversion associated nucleotide #5742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
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ID ADIS1144 standard; DNA; 17 BP.
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                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-441574/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potentially useful
                                                                                                                                                                                                                                                                 WO2003040369-A2
                                                                                                                                                                                                                            Homo sapiens.
                                                     18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telerman A,
                                                                                                                               cytostatic;
                                                                                                                                                                                                                                                                                                     15-MAY-2003
                                                                                                                                                                                        diagnosis.
                 ADB45419;
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Matches
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Gaps

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ADB45419 standard; DNA; 17 BP.

RESULT 48 ADB45419/c ID ADB45

47 AAAGAGCCAGCGAAG 61

14; Conservative

Matches

AATGAGCCAGCGAAG 1

15

셤

Homo

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New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          es; probe; myosin-like protein-1; hGDMLP-1;
-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an isolated nucleic acid sequence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.4%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 61; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GDMLP-1 probe SEQ ID NO:10028
                                                                                                                                                                                                                                     Amson R;
                                                                                                                                                                                          (MOLE-) MOLECULAR ENGINES LAB SA.
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 612; 798pp; French
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2001WO-US000662.
2001WO-US000663.
2001WO-US000665.
2001WO-US000665.
2001WO-US000665.
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2000US-0236359P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 TGGAGTCCTCTGAGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                   Puijnder M, Telerman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hGDMLP-1 agonist hGDMLP s
skeletal muscle function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAGTCTTCTGAGA
                                                                                                                                                                                                                                                                                WPI; 2003-250498/25.
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30-JAN-2001;
30-JAN-2001;
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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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27-SEP-2000;
04-OCT-2000;
                      FR2826373-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
                                                            27-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN73126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, 88
hGDMLP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACN73126
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                                                            tumour suppression; tumour reversion; apoptosis; virus resistance;
cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
primer; PCR; gene chip; antisense; viral disease; tumour;
cell degeneration; cancer; Alzhaimer's disease; schizophrenia; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistence to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful seprobes and primers for detecting, indentifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant playmanceuticals for prevention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The sequence is that of a nucleic acid sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to novel isolated nucleic acid sequences involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
                 Human tumour suppression/reversion-related DNA sequence SeqID3647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.4%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 61;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/publishedpct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3647; 30pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour suppressor sequence #2477.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACC53710 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                    17-SEP-2002; 2002WO-IB004523.
                                                                                                                                                                                                                                                                                                                                               17-SEP-2001; 2001FR-00011980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 TGGAGTCCTCTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-313354/30.
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Les 14; Conserv
                                                                                                                                                                                                              #02003025177-A2
                                                                                                                                                                      sapiens
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RESULT 50 ACC53710/

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Query Match

Matches

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Gaps

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WPI; 1994-048873/06.
                                      WPI; 1994-048873/06
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(STRA-) STRATAGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9402615-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                            LCR Oligo D.
                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
22-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mathur EJ,
                    Mathur EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                            AAQ55744;
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                               AAQ55744
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                                                                                                                                                                                                                                              The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and 65% identity to (S1). A polypeptide of the invention acts as a agonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                                                             Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                        Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu; hyperthermophilic archaebacterium; catalysis; blunt-end; Tth;
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                        17.4%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 61; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                   invention for scanning the sequence represented in ACN63103
                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                        Rank D,
                                                                                                                                                                                                                              Disclosure; SEQ ID NO 10028; Opp; English.
                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
        30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000670.
05-FEB-2001; 2001US-0266860P.
25-MAY-2001; 2001US-00866108.
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 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGAGTCCTCTGAG 42
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AAQ55741 standard; DNA; 18
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermus thermophilus; ss
                                                                                                                                       Ji Y, Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                            WPI; 2004-533378/51.
                                                                                                                    SHANNON M E.
                                                                             PENN S G.
HANZEL D K.
                                                                                                   RANK D.
CHEN W.
                                                          98 Y.
30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1993;
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22-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCR Oligo A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ55741;
                                                                                                                                                                                                            function.
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                           (CHEN/)
                                                           (duxy/)
                                                                     (JIYY/)
                                                                                        HANZ/)
                                                                                                  RANK/
                                                                                                                                        3u Y,
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Four oligonucleotide probes (AAQS5741-44) and two oligonucleotide templates (AAQS5739-40) were used in a ligase chain reaction of seconbinant bfu DNA ligase. The assey shows that both Tth DNA ligase and Pfu DNA ligase perform well in LCR after multiple cycles forming a single LCR DNA fragment without appreciable blunt-end ligation or background exaction prods. However, the Tth DNA ligase in not heat stable when exposed to temps. required to separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                            Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation specificity and stability at high temperatures, giving greater efficiency in ligase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation specificity and stability at high temperatures, giving greater efficiency in ligase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu;
hyperthermophilic archaebacterium; catalysis; blunt-end; Tth;
Thermus thermophilus; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
Schoettlin WE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schoettlin WE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 12; Page 56; 84pp; English.
                                                                                                                                                                                                                                                               Example 12; Page 56; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 GGACACATGGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ55744 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 83.3
Marsh EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marsh EJ,
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Wed Apr 19 16:15:55 2006

RESULT 55

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid contg. gene for thermostable DNA ligase - useful in ligase chain reactions, stable up to 100 deg. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        separate the strands of double-stranded genomic DNA. (Updated on 25-WAR-2003 to correct PF field.)
LCR DNA fragment without appreciable blunt-end ligation or background reaction prods. However, the Tth DNA ligase in not heat stable when exposed to temps. required to separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;
                                                                                                                                                ö
                                                                                                                DB 1; Length 18;
                                                                                                                                                3; Indels
                                                                                Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                            17.1%; Score 13.2; D
83.3%; Pred. No. 69;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Oligo A probe for Pfu DNA ligase LCR assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCR; template dependent ligation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marsh EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 12; Col 25-26; 29pp; English.
                                                                                                                                                                               35
                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                        93US-00096947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-00919140.
                                                                                                                                                                               18 GGATACAACTCTGGAGTC
                                                                                                                                                                                                              1 GCACACAACCTTGGAGTC
                                                                                                                                                Conservative
                                                                                               Query Match
Best Local Similarity (
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Recombinant Pyrococcus furiosus (Pfu) DNA ligase (AAR96967) activity was assayed in a ligase chain reaction (LCR). The DNA templates consist of two complementary 36-mer synthetic oligonucleotides (AAT14931). The probes consist of 18-mer oligonucleotides (ReAT14931). The results illustrated that both Tth and Pfu DNA figase perform will in LCR after multiple cycles forming a single LCR DNA fragment without appreciable blunt-end ligation or background reaction products. Pfu DNA ligase was able to perform well in LCR without a "pre-melting" step, whereas Tth DNA ligase produced no detectable LCR product indicating that the Tth DNA ligase is not heat stable when exposed to temperatures required to separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid contg. gene for thermostable DNA ligase - useful in ligase chain reactions, stable up to 100 deg. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transmembrane serine protease; membrane-type serine protease; MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic;
                                                                                                                                                 thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;
LCR; template dependent ligation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 13.2; D 83.3%; Pred. No. 69; tive 0; Mismatches
                                                                                                                   Oligo D probe for Pfu DNA ligase LCR assay.
                                                                                                                                                                                                                                                                                                                                                                               Marsh EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Col 25-26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35
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              ВР
                                                                                                                                                                                                                                                                                     93US-00096947.
                                                                                                                                                                                                                                                                                                                  92US-00919140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GGATACAACTCTGGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACACAACCTTGGAGTC
              AAT14937 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                               Schoettlin WE, Mathur EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD13161 standard; DNA; 18
                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-200280/20.
                                                                                                                                                                                                                                                                                                                                                 (STRA-) STRATAGENE
                                                                                                                                                                                                                                                                                                                  23-JUL-1992;
                                                                                                                                                                                                                                                                                     22-JUL-1993;
                                                                       25-MAR-2003
26-SEP-1996
                                                                                                                                                                                                                         JS5506137-A
                                                                                                                                                                                                                                                       09-APR-1996
                                                                                                                                                                                              Synthetic.
                                          AAT14937;
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Gaps ö

3; Indels

DB 1; Length 18;

Score 13.2; DE Pred. No. 69; 0; Mismatches

17.1%;

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15; Conservative

Query Match Best Local Similarity Matches 15; Conserva

35

18 GGATACAACTCTGGAGTC

GGACACAACCTTGGAGTC 1

18

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ADA25180/
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                                                                                                                                                                                                                                                                                                                                                                                  corresponding nucleotides and the protease domain of a type-II membrane-
type serine protease (MTSP). MTSP is useful for identifying compounds
type serine protease (MTSP). MTSP is useful for identifying compounds
medicament for treating neoplastic disease. MTSP and its corresponding
nucleotides are useful in preventing or treating tumours or cancers such
as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in
diagnostics and in hybridisation assays. MTSP is useful as a diagnostic
marker for tumour development, growth and/or progression and as
immunogens to generate antibodies that specifically bind to it. MTSP DNA
is useful in a yeast two-hybrid system and in gene therapy. The present
sequence is a gene-specific RACB (rapid amplification of cDNA ends) PCR
primer used to obtain 5' region of cDNA encoding protease domain of MTSP1
                                                                                                                                                                                                                                                                                                  Novel single chain polypeptide comprising protease domain of type-II membrane-type serine protease or its catalytically active portion useful for treating and preventing cancer and tumor.
 colon adenocarcinoma; ovarian carcinoma; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; amide derivative; serine protease; matriptase; MTSP1; cancer; therapy; tumour; metastasis; cytostatic; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                            The invention relates to transmembrane serine proteases and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MTSP1 protease domain cDNA amplifying sense PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.1%; Score 13.2; DB 1; Length 18; 83.3%; Pred. No. 69; ive 0; Mismatches 3; Indels
           rapid amplification of cDNA ends; RACE; PCR primer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 164; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GGAGTCCTCTGAGAGGTA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                   03-FEB-2000; 2000US-0179982P.
18-FEB-2000; 2000US-0183542P.
22-JUN-2000; 2000US-021314P.
26-JUL-2000; 2000US-020970P.
08-SEP-2000; 2000US-00657986.
                                                                                                            02-FEB-2001; 2001WO-US003471
                                                                                                                                                                                                 22-SEP-2000; 2000US-0234840P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                         (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                  Ong EO,
                                                                                                                                                                                                                                                                           WPI; 2001-488877/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
lung carcinoma;
                                                            WO200157194-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200220475-A2
                                     Homo sapiens
                                                                                                                                                                                                                                                  Madison EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-2002
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                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
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XX
AC AAD3
XXX
AC AAD3
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DT 21-A
XXX
KW Humg
XW Thei
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CS HOM
XXX
CS HOM
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB; Serine protease; matriptase; MTSP1; cancer; tumour; colon cancer; lung cancer; stomach cancer; rectal cancer; skin cancer; human; protease domain; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                  Amide derivatives, useful as serine protease inhibitors for reducing
                                                                                                                                             Ong EO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                             Semple JE, Coombs GS, Reiner JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.1%; Score 13.2; I
83.3%; Pred. No. 69;
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                           tumor progression and metastasis.
                                                                                                                                                                                                                                                                                                                                           Example 1; Page 43; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA25180 standard; DNA; 18 BP
07-SEP-2001; 2001WO-US028137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-2002; 2002US-00092004.
                                                08-SEP-2000; 2000US-00657986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MTSP1 sense PCR primer.
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07-SEP-2001; 2001WO-US028137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 GGAGTCCTCTGAGAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGTCGTAGGAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 83.3
                                                                                                                                           Madison EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coomba GS,
                                                                                             (CORV-) CORVAS INT INC
                                                                                                                                                                                                                  WPI; 2002-415722/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMPLE J E.
COOMBS G S.
REINER J E.
ONG E O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPI; 2003-625421/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003050251-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
                                                                                                                                           Duncan DF,
Araldi GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA25180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEMP/)
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Matches
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The invention relates to a method of treating a condition ameliorated by an inhibition or decrease in serine protease activity of matriptase or MTSP1 which comprises administration of a peptide containing compound. The compound is useful for treating pathological conditions ameliorated by decreasing or inhibiting serine protease activity of matriptase or MTSP1, for the treatment of cancerous conditions, e.g. cancerous tumours, colon cancer, lung cancer, stomach accer, rectal cancer or skin cancer. The present sequence represents the human MTSP1 sense PCR primer.
Treatment of condition ameliorated by inhibition of serine protease activity of matriptase, e.g. cancerous tumors, retard metastasis or cancer of lung, colon and stomach, comprises administration of a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                 Example 1; Page 14; 34pp; English.
                                                                                          containing compound
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Score 13.2; DB 1; Length 18; Pred. No. 69; 0; Mismatches 3; Indels ö 47 ch 17.1%; il Similarity 83.3%; 15; Conservative ( 30 GGAGTCCTCTGAGAGGTA Best Local Similarity Query Match Matches 8

GGAGTCGTAGGAGAGGTA 1

18

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ADM57469 standard; DNA; 18 03-JUN-2004 ADM57469; ADMS 7469,

(first entry) 

M. tuberculosis PCR primer RD3-int-REP.R.

antibacterial; vaccine; mmpL6; Mycobacterium; BCG; TbD1; ss; PCR; primer. Mycobacterium tuberculosis

BP1338657-A1

27-AUG-2003.

25-PBB-2002; 2002BP-00290458

25-PEB-2002; 2002EP-00290458

(INSP ) INST PASTEUR

New TbD1 nucleic acids having the mutation CTG to CGG at codon 463 of gene katG, useful for distinguishing Mycobacterium tuberculosis infection from M africanum, M. canetti, M. microti, M. bovis, or M. bovis BCG WPI; 2003-699254/67.

Garnier T;

Biglmeier K,

Brosch R, Gordon S,

Cole S,

Disclosure; Page 19; 73pp; English

infection

The invention relates to a novel isolated or purified nucleic acid. A polypeptide encoded by a nucleic acid of the invention has antibacterial activity, and may have a use in a vaccine. The nucleic acid is a TbD1 nucleic acid having a fully defined sequence of 3953 bp given in the specification. The TbD1 deletion or mmpL6 551 polymorphism is useful as a genetic marker for the differentiation of Mycobacterium strain of M. tuberculosis complex. The genetic marker in association with at least one genetic markers selected from RD1, RD2, RD3, RD4, RD5, RD6, RD7, RD8, RD9, RD10, Rd11, RD13, RD14, RVD1, RVD3, RVD4, RVD5, RD6, RD7, RD8, SyrA95, oxyR'285, and pncA57, may be used for the differentiation of Mycobacterium strain of M. tuberculosis complex. The nucleic acids may

also be used to distinguish an infection resulting from M. tuberculosis from an infection resulting from M. africanum, M. canetti, M. microti, M. bovis, M. bovis BCG. The present sequence is used in the exemplification of the invention. 8888888

Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Gape ö DB 1; Length 18; Indels . . 17.1%; Score 13.2; E 83.3%; Pred. No. 69; tive 0; Mismatches Conservative Local Similarity les 15; Conserv Query Match Matches

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53 н 18 AAGATCGCCTGGGGGTAC 6 AAGACGGCCTGGGGATAC a ò

RESULT 60 ADJ82396

ADJ82396 standard; DNA; 15

ADJ82396;

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Gaps

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(first entry) 06-MAY-2004

KLMSY-encoding nucleotide #124.

BB; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;

angiogenesis

Synthetic.

WO2003045973-A2

05-JUN-2003

30-SEP-2002; 2002WO-US031165.

28-NOV-2001; 2001US-033476P

(BECT ) BECTON DICKINSON & CO (HAAL/) HAALAND P D.

Spargo CA; Heidaran M, Dean C,

WPI; 2003-505179/47

New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

Disclosure; SEQ ID NO 177; 48pp; English.

The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growt not plot. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys (P1) App-AspGlu-Glu-Lys (P2) Lys-Luwet-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cellys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cellysarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (anglogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide 

Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10023.
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Score 13; DB 1; Length 15;
Pred. No. 60;
                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 10023; 214pp; English
                         100.0%; Prea. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000; 2000US-02345879; 27-SEP-2000; 2000US-02345879; 27-SEP-2000; 2000US-02345879; 27-SEP-2000; 2000US-02345879; 20-DAN-2001; 2001WO-US000661; 30-JAN-2001; 2001WO-US000666; 30-JAN-2001; 2001WO-US000666; 30-JAN-2001; 2001WO-US000666; 30-JAN-2001; 2001WO-US000666; 30-JAN-2001; 2001WO-US000666; 30-JAN-2001; 2001WO-US000666; 30-JAN-2001; 2001WO-US000669; 30-JAN-2001; 2001WO-US0006700.
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          16.9%;
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                                                                                                                                           71
                                                                                                                                                                                                 AAGCTGATGTCCT 13
                                                                       13; Conservative
                                                                                                                                               59 AAGCTGATGTCCT
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                                       Local Similarity
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          Query Match
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ABN10031 6

ABN1003 6

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production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGPMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel myosin-like protein-1, useful for treating or preventing disorder
                                                                                                                                                                                                                                                                                                                                                                   Human; 88; probe; myosin-like protein-1; hGDMLP-1;
hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
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                                                                                                                                               DB 1; Length 17; 70;
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                                                                                                                         Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
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                                                                                                                                              Match 16.9%; Score 13; DB Local Similarity 100.0%; Pred. No. 70; les 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Human GDMLP-1 probe SEQ ID NO:10023.
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2001WO-US000662.
2001WO-US000663.
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2000US-0236359P.
2000GB-00024263.
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2001WO-US000667
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                                                                                                                                                                                                                                                                              ACN73121 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                              02-DEC-2004 (first entry)
                                                                                                                                                                                               27 TCTGGAGTCCTCT 39
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                                                                                                                                                                                                           Ji Y, Penn SG,
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HANZEL D K.
RANK D.
CHEN W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004137589-A1
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30-JAN-2001;
30-JAN-2001;
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30-JAN-2001;
30-JAN-2001;
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27-SEP-2000;
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(CHEN/)
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Matches
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                                                                                                    The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and 55% identity to (S1). A polypeptide of the invention acts as a agonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes a facilitative glucose transporter protein, GLUT9, and its functional fragments. Agents that inhibit activity or expression of GLUT8 (particularly non-utilizable glucose analogues, antisense sequences or dominant negative mutants) are used to treat malignancy, particularly cancer of breast, prostate and epithelial cells (e.g. skin or colon). Agents that upregulate expression of GLUT8 (e.g. the GLUT8 gene, administered by tissue-localized gene therapy) are used to treat non-insulin-dependent diabetes mellitus and/or insulin
genome-derived
associated with decreased expression or activity of human genome-derive myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Facilitative glucose transporter protein; GLUT8; malignancy; breast cancer; prostate cancer; epithelial cell cancer; one-insulin-dependent diabetes mellitus; insulin resistance; central obesity; hypertension; dyslypidaemia; glucose intolerance; cancer; 3684 gene; PCR primer; ss.
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                                                                                                                                                                                                                                                                                         invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer used to amplify 36B4 gene (in control reactions)
                                                                                                                                                                                                                                                                                                                                                             Score 13; DB 1; Length 17; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding a facilitative glucose transporter.
                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                       Disclosure; SEQ ID NO 10023; Opp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX35522 standard; cDNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-AU000819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGGAGTCCTCT 39
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                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1998;
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resistance (e.g. central obesity, hypertension, dyslypidaemia or glucose intolerance). Detecting expression of GLUT8 is used for diagnosis, monitoring and staging of cancers, particularly of the breast. Antibodies raised against GLUT8 are useful as immunoassay reagents and as therapeutic inhibitors. PCR primers AAX35521-22 were used in the course of the invention
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                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sø; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
NHBLP1; passive replacement therapy; vaccine; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Na/H exchanger-like protein 1 gene oligonucleotide #889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic methods. This sequence corresponds to a 17-mer (spanning the sequence of the human NHELP1 gene (ADC03514).
                                                                                                                                                              DB 1; Length 18;
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                                                                                                                                   Sequence 18 BP; 1 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                   100.0%; Prec. ...
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                                                                                                                                                                    16.9%; Score 13;
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ID ADC04442 standard; DNA; 17 BP.
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23-MAY-2001; 2001US-00864761.
21-DEC-2001; 2001US-0343331P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                            62
                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                            50 GAGCCAGCGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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DB 1; Length 17;

16.6%; Score 12.8;

Query Match

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fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis
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                                                                                                                                                                                                                                                                                                                                  cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                      Gaps
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                                                                                                                                                                                                                                                                                                Tumour suppression/reversion associated nucleotide #5659.
                      Indels
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   Pred. No. 75;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression of the nucleotides
                                                                                                                                                                                     ADB45336 standard; DNA; 17 BP
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87.5%;
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87.5%;
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                                                                                                                                                                                                                                                            (first entry)
                                                         AAGAGCCAGCGAAGCT
                                                                                           17 ATGAGCCAGCGAAGAT
   Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            diagnosis.
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                                                                                                                                                   RESULT 65
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The present sequence was used to isolate a cDNA fragment of the chick seven transmembrane receptor R35 by RNA fingerprinting. R35 is useful for treating neuropathic pain, inflammatory and chronic pain, incontinence, and disorders of the gastrointestinal tract associated with gut motility and secretion such as irritable bowel syndrome. It is also useful for inducing an immune response in a mammal to protect against the diseases. It is useful in screening assays to identify compounds which stimulate or inhibit the function of the polypeptide, to identify membrane bound or solubbe receptors and also for the structure-based design of an agonist, antagonist or inhibitor of R35
                                                                                                                                                                                                  Chick; R35; uropathic; antiinflammatory; analgesic; gene therapy; seven transmembrane receptor; neuropathic pain; inflammation; incontinence; irritable bowel syndrome; RNA fingerprinting; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel R35 polypeptides and polynucleotides useful for treating neuropathic, inflammatory and chronic pain, incontinence and irritable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 2 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                     Chick R35 RNA fingerprinting primer P3.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINB BEECHAM PLC. (PLAC ) MAX-PLANCK INST NEUROBIOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Friedel R, Michalovich D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 23; 55pp; English.
                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                          20-APR-2000; 2000WO-GB001546.
                                                                                                                                                                                                                                                                                                                                                                                                        99GB-00009161.
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                                                                             AAC68677 standard; DNA; 18
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17 AAGGCTGCCTGGGGAT
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                                                                                                                                        (first entry)
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Best Local Similarity 87.59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-679669/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bowel syndrome.
                                                                                                                                                                                                                                                                                                             WO200064928-A2
                                                                                                                                                                                                                                                                                Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuropathic,
                                                                                                                                        22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stubbusch J;
                                                                                                                                                                                                                                                                                                                                             02-NOV-2000
                                                                                                           AAC68677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG14616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ×
                                                                                                                                                                                                    Chick;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barde
                                                                                                                                                                                                                      seven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 67
                                                RESULT 66
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14; Conservative

Local Similarity

Query Match Matches

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Gaps

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2; Indels

0; Mismatches

Human cancer suppressing protein associated PCR primer. ss; PCR; human; cancer suppression; cancer; primer.

Homo sapiens

CN1403478-A.

19-MAR-2003

(first entry)

20-MAY-2004

ADL25789;

ADL25789 standard; DNA; 18 BP

ADL25789

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Therapeutic response, therapeutic outcome, interferon-alpha-2b; ribavirin; hepatitis C virus; HCV infection; interleukin-10; IL-10 regulatory region; single mucleotide polymorphism; SNP; haplotype; genotype; cytotoxic T-1ymphocyte antigen-4; CTLA-4 promoter; CTLA-4 exon 1; bacterial infection; meningococcal infection;
                                                                                                                                                                                                                                                                                  Predicting a therapeutic response comprises comparing a first nucleic acid allele in an interleukin-10 (IL-10) regulatory region with a second nucleic acid allele in the IL-10 regulatory region associated with a
                                                                         rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;
Inflammatory bowel disease; multiple sclerosis; human; PCR; primer; ss.
Human CTLA-4 exon 1 reverse PCR primer, SEQ ID NO:7.
                                                                                                                                                                                                                                        Van Leeuwen DJ
                                                                                                                                                                                                                                                                                                                                        Claim 41; SEQ ID NO 7; 34pp; English.
                                                                                                                                                                        27-FEB-2002; 2002WO-US006207.
                                                                                                                                                                                            27-FEB-2001; 2001US-0271811P
                                                                                                                                                                                                                                        Kaslow RA,
                                                                                                                                                                                                                   (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                              WPI; 2002-707021/76.
                                                                                                                                                                                                                                       Tang J,
                                                                                                                              WO200268699-A1.
                                                                                                                                                                                                                                                                                                                    known outcome
                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                      Yee L,
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The invention relates to a method for predicting an individual's therapeutic response to the administration of interferon-alpha-2b and ribavirin for the treatment of a pathological condition, especially hepatitis C virus (HCW) infection. The method involves determining which allelic form is present at positions -3575, -2763, -1082, -819 and -592 of the interleukin-10 (IL-10) regulatory region, and comparing these with the allelic forms at these positions which are associated with a known cutcome of interferon-alpha-2b and ribavirin administration. Presence of the single mucleotide polyworphisms -592A, e197 as a haplotype, concompassing positions -3575, -2763, -1082, -081977 genoxypes, the combination of -592A, e197 as a genotype, or possession of the (108) TCATA haplotype (ancompassing positions -3575, -2763, -1082, -0819 and -592) is associated with a sustained response to interferon-alpha condition thereof primers to this therapy. In contrast, the presence of -592C and -819C, or the (108) TCATA haplotype indicates that the patient will be non-responsive to this therapy. The method optionally further comprises detection of the allele at position -318 of the cytotoxic T-lymphocyte antigen-4 (CTLA-4) promoter and the allele at position 49 of exon 1 of the CTLA-4 gene. The invention also encompasses kits and oligomucleotide primers for use in the methods of the invention. The method and primers care useful for identifying and analysing genetic polymorphisms in the IL-10 regulatory region and/or cyctocake T-lymphocyte antigen-4 (CTLA-4) promoter and the allele at position in pathological condition, or for predicting the outcome of therapputic intervention in pathological conditions such as bacterial infection), rheumatoid arrhitials systemic lupus erythematosus, 3jogren's syndrome, inflammatory bowel disease or multiple erythematosus. The present sequence is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 7 A; 7 C; 4 G; 0 T; 0 U; 0 Other;
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Gaps

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suppressing function, polymiclectides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the method of using the polypeptide. The present invention also discloses the aconcer. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present the nument on also discloses the application of the polypuclection aconcer suppressing function. The present the human protein with cancer suppressing function. The present sequence represents a human cancer suppressing protein associated PCR primer.

invention relates to one kind of human protein with

Disclosure; Page 12; 43pp; Chinese.

coding sequence.

Human protein with function of suppressing cancer cell growth and its

WPI; 2003-494227/47.

Yang S;

Gu J,

(SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.

12-SEP-2001; 2001CN-00126726. 12-SEP-2001; 2001CN-00126726.

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Human; 88; PCR; primer; Allele specific primer; coronary stenosis; angina; ischaemic chest pain; myocardial infarction; sudden cardiac death; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allele specific primer B for human stenosis marker hCV25612829.
                                                                                                                                                                                                                                                                                                                             Query Match
16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 6 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 ADR74794 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                            AAGACGCATAGGGAT 18
                                                                                                                                                                                                                                                                                                                                                             6 AAGACGCCTGGGGAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                ADR74794;
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0; Mismatches

62

47 AAAGAGCCAGCGAAGC

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1 ACAGAGCCAGCCAAGC 16

79;

16.6%; Score 12.8; 87.5%; Pred. No. 79

Query Match
Best Local Similarity 87.5
Matches 14; Conservative

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The invention relates to identifying an individual who has altered risk for developing coronary stenosis comprising detecting a single nucleotide polymorphism (SNP) in any one of the 67073 nucleotide sequences (not given in the specification), in the individual's nucleic acid acids, where the gresnece of the SNP is correlated with an altered risk for stenosis in the individual. Also included are an isolated nucleic acid molecule (comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP as cited above, or their complement), an isolated polypeptide comprising an amino acid sequence selected from any of the 569 amino acid sequences (not defined in the specification), an antibody that specifically binds to the polypeptide containing the SNP as cited (where the amplified polymucleotide containing the SNP as cited (where the amplified polymucleotide containing the SNP as cited (where the amplified polymucleotide is between about 16 and about 1,000 concleted caid molecule containing the SNP as the for detecting a variant polypeptide and identifying an agent useful concletion, detecting a variant polypeptide and identifying an agent useful contecting, detecting a variant polypeptide and identifying an agent useful contecting probe hybridisation, allele specific primer extension, allelesspecific amplification, sequencing, 5' nuclease digestion, and lead to sugariation, allele specific primer extension, allelessed signation, and and unidividual who has altered isk for developing coronary stenosis, and ultimately sudden cardiac death. The present sequence is an allele specific primer for amplifying a SNP containing region of a human marker gene associated with stenosis. NOTE: SEQ ID 1-67771 are not shown in the specification but are provided on a CD-R named CLOOISIOCDR which was not supplied with the specification.
                                                                                                                                                                                                                                                                                                                            Identifying an individual who has altered risk for developing stenosis comprises detecting single nucleotide polymorphism (SNP), in the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; SEQ ID NO 68106; 146pp; English.
                                                                                                                                                                                                                                      Luke MM;
                                                                    10-MAR-2004; 2004WO-US007140.
                                                                                                                10-MAR-2003; 2003US-0453050P.
30-APR-2003; 2003US-0466437P.
                                                                                                                                                                                                                                      Devlin JJ,
                                                                                                                                                                                     (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                  WPI; 2004-668949/65.
                      23-SEP-2004.
                                                                                                                                                                                                                                      Cargill M,
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Gaps ö DB 1; Length 18; 2; Indels Seguence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 U; 0 Other; 16.6%; Score 12.8; D 87.5%; Pred. No. 79; Live 0; Mismatches 14; Conservative Local Similarity Query Match Matches

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7 GCCAAGATGATGTCCT 18 GCGAAGCTGATGTCCT 셤 à

ADV37028 standard; RNA; 15 (first entry) 10-FEB-2005 ADV37028; RESULT 70 ADV37028
ID ADV3
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XX
AC ADV3
XX
XX
DT 10-F
DE Huma
XX
KW Enzy

Enzymatic nucleic acid molecule; gene expression; down regulation; Human anti-HER2 NCH ribozyme substrate sequence #907.

MetAP-2; human telomerase; hTBRT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; breat cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; 

Homo sapiens.

WO200116312-A2

08-MAR-2001

30-AUG-2000; 2000WO-US023998

99US-0151713P. 99US-016643. 99US-015626P. 99US-00436430. 99US-0169100P. 99US-0044432. 30-DEC-1999; 99US-00476387. 04-FEB-2000; 2000US-00498824. 20-MAR-2000; 2000US-00531025. 2000US-0197769P 06-DEC-1999; 29-DEC-1999; 29-DEC-1999; 14-APR-2000; 31-AUG-1999 27-SEP-1999 08-NOV-1999

(RIBO-) RIBOZYME PHARM INC.

2000US-00578223

23-MAY-2000;

09-AUG-2000; 2000US-00636385

Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Chowrira B; Beaudry A, Zinnen S, Lugwig J, Sproat BS; Mcswiggen J, U Karpeisky A, M Stinchcomb D,

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 7; Page 490; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (MTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HERA/C-erb2/neu), phospholamban (PLM), presentlin-1 (ps-1), presentlin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleid end calcules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, disbetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocallular cardinoma. The anzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have Note: Some SEQ ID different sequences associated with them

Sequence 15 BP; 3 A; 5 C; 4 G; 0 T; 3 U; 0 Other;

Score 12.4; DB 1; Length 15; Pred. No. 75; 16.1**%**; 71.4**%**; Query Match Best Local Similarity

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                                                                                                                                                                                                                                                     Enzymatic nucleic acid molecule; gene expression; down regulation, protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase Calpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; beast cancer; Alzheimer's disease; disease; bepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C apipa (PKC alpha), beta-secretase (BACB), human spidermal growth factor receptor-2 (HERZ/c-erbZ/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Chowrira
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                          Human Her2 class II (zinzyme) ribozyme substrate sequence #506.
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 1; Indels
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 16; Page 633; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usman N, Blatt L,
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99US-00406643.
99US-0156236P.
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99US-00436430.
99US-0169100P.
99US-00474432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-00636385
                                                                                                                                   ADV64524 standard; RNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC.
                                              CUGGAGCCCUCUGA 14
                               CTGGAGTCCTCTGA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         obesity and heart disease.
                                                                                                                                                                                             (first entry)
 10; Conservative
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Karpeisky A, M
Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200116312-A2
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29-DEC-1999;
30-DEC-1999;
04-PEB-2000;
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                                                                                                                                                                                              10-FEB-2005
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09-AUG-2000;
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06-DEC-1999;
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                                                                                                                                                                 ADV64524;
                               28
 Matches
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nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepaticis can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, genome-derived myosin-like protein 1, GDMLP-1, hGDMLP-1, heart, muscle, myosin, chromosome 22, gene therapy, vaccine, heart disease, skeletal muscle disorder, amplicon, screening, ss.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10029
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                                                                                                                                                                                                                                                             ch 16.1%; Score 12.4; DB 1; Length 17; Similarity 71.4%; Pred. No. 86; 10; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                               Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN10037 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0235359
2000US-0235359
2001WO-US000661
2001WO-US000663
2001WO-US000663
2001WO-US000664
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2001WO-US000668.
2001WO-US000669.
2001WO-US000670.
2001US-0266860P.
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cugangcccucuca 17
                                                                                                                                                                                                                                                                                                                            28 CTGGAGTCCTCTGA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ji Y, Penn SG,
                                                                                                                                                                                                  associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-179446/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AEOM-) ABOMICA INC
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200192524-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000;
30-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
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                                                                                                                                                                                                                                                              Query Match
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Matches
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Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
Disclosure; SEQ ID NO 10029; 214pp; English
                                                                                                                                                                                                                                                                                                                                               Human HER2 DNAzyme substrate #786.
                                                                                                                                                                                                                                                                                                ABZ65329 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2001; 2001US-0294140P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2002; 2002WO-US016840
                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2001; 2001US-0296249P
10-SEP-2001; 2001US-0318471P
                                                                                                                                                                                                                    Local Similarity 92.9%;
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                           29 TGGAGTCCTCTGAG 42
                                                                                                                                                                                                                                                          recaercerere 14
                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen J;
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                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                ABZ65329
                                                                                                                                                                                                                                                                                  RESULT 73
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acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ55889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66530 - ABZ66534, ABZ665310 - ABZ66534, ABZ66530 - ABZ66534, ABZ66530 - ABZ66534, ABZ665310 - ABZ66 The invention relates to a novel short interfering RNA (siRNA) nucleic 16.1%; Score 12.4; DB 1; Length 17; 71.4%; Pred. No. 86; Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other; Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative ribozymes of the invention 28 CTGGAGTCCTCTGA 41 |:|||| ||:||| 4 CUGGAGCCCUCUGA 17 WPI; 2003-302724/30. (ABOM-) AEOMICA INC EP1273660-A2. Homo sapiens. 18-DEC-2003 08-JAN-2003 ADC04446; ADC04446/c Gu Y; RESULT 74 \* 8 The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used as probes to detect, characterise and quantify nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser describin in instation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO ö Gaps Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss. ö 16.1%; Score 12.4; DB 1; Length 17; 1; Indels Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequence Pred. No. 86; 0; Mismatches

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Gaps

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1; Indels

3, Mismatches

The invention relates to a nucleic acid molecule which encodes a Na+/H+ exchanger like protein (NHELPI). The NHELPI nucleic acid molecule, NHELPI polypeptide, an antibody against the protein or its antigen-binding fragment is useful in therapy. The NHELPI nucleic acid molecule, NHELPI polypeptide and an agonist are particularly useful for manufacturing a medicament for treating or preventing a disorder associated with decreased expression or activity of human NHELPI. The antibody or its antigen-binding fragment, and an antagonist, are useful for manufacturing a medicament for treating or preventing a disorder associated with increased expression or activity of human NHELPI. The NHELPI nucleic acid ಹ New human sodium-hydrogen exchanger like protein 1 (NHBLP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein; NHELP1; passive replacement therapy; vaccine; diagnosis. Human Na/H exchanger-like protein 1 gene oligonucleotide #893. Example 2; SEQ ID NO 933; 468pp; English. ВР. 30-JAN-2001; 2001WO-US000666. 23-MAY-2001; 2001US-00864761. 21-DEC-2001; 2001US-0343331P. 25-JAN-2002; 2002EP-00001160. ADC04446 standard; DNA; 17 (first entry) NHELP1 

Claim 4; Page 148; 185pp; English

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GAGCCAGCGAAGCT

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or protein is useful as passive replacement therapy, as a vaccine, or in diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide spanning the sequence of the human NHELP1 gene (ADC03514).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein; NHELP1; passive replacement therapy; vaccine; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Na/H exchanger-like protein 1 gene oligonucleotide #888.
                                                                                                               DB 1; Length 17;
                                                                                                                                                     1; Indels
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                                                                          Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                             / Match 16.1%; Score 12.4; I Local Similarity 92.9%; Pred. No. 86; nes 13; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                         ADC04441 standard; DNA; 17 BP
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23-MAY-2001; 2001US-00864761.
21-DEC-2001; 2001US-0343331P.
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                                                                                                                                                                                                                                                                                                                                                               ADC04441;
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The invention relates to a nucleic acid molecule which encodes a Na+/H+ exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1 polypeptide, an antibody against the protein or its antigon-binding fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1 polypeptide and an agonist are particularly useful for manufacturing a medicament for treating or preventing a disorder associated with antigen-binding fragment, and an antagonist, are useful for manufacturing a medicament for treating or preventing a disorder associated with increased expression or activity of human NHELP1. The NHELP1 numanated with increased expression or activity of human NHELP1. The NHELP1 nucleic acid or protein is useful as passive replacement therapy, as a vaccine, or in diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide spanning the sequence of the human NHELP1 gene (ADC03514).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as passive replacement therapy or as a vaccine for treating or preventing disorders associated with aberrant expression or activity of human
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                                                                                                                                                                                                                            88; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
NHELP1; passive replacement therapy; vaccine; diagnosis.
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                                                                                                                                                                                           Human Na/H exchanger-like protein 1 gene oligonucleotide #887.
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23-MAY-2001; 2001US-00864761.
21-DEC-2001; 2001US-0343331P.
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                                                                                       ADC04440 standard; DNA; 17
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                                                                                                                                                        18-DEC-2003 (first entry)
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 GAGCCAGCGAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                        ADC04440;
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                                                    RESULT 76
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Gaps

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16.1%; Score 12.4; DB 1; Length 17; 92.9%; Pred. No. 86; tive 0; Mismatches 1; Indels

13; Conservative

Query Match Best Local 8

Matchee

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tumour suppression; tumour reversion; apoptosis; virus resistance;
gytostatic; viruoide; neuroprotective; nootropic; neuroleptic; probe;
primer; PCR; gene chip; antisense; viral disease; tumour;
cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses. The invention may be useful for the development of compounds with a cytostatic, virucide, neuroprotective, nootropic or neuroleptic activity. The DNA sequences may be useful as probes and primers for detecting, indentifying, quantifying and/or amplifying nucleic acid, for example as one component of a gene chip, in vitro as antisense reagents and for production of recombinant opphypaptides. The invention may therefore be useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. The present sequence is that of a nucleic acid sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel isolated nucleic acid sequences involved
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diabetic retinopathy; age related macular degeneration;
angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing;
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                                                     Human tumour suppression/reversion-related DNA sequence SeqID316.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          Tuijnder M;
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                                                                                                                                                                                                                                                                                                                                               17-SEP-2001; 2001FR-00011980.
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                 (first entry)
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                                                                                                                                                                                                                               WO2003025177-A2
                                                                                                                                                                                           Homo sapiens
                   15-APR-2004
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menstruation disorder; premenstrual syndrome; menopause; Gynecological; Cytostatic; Ophthalmological; Antidiabetic; antiangiogenic; Antipsoriatic; Antirheumatic; Antiarthritic; Vulnerary; Hemostatic; Contraceptive; 85; enzymatic nucleic acid. endometriosis; endometroid carcinoma; gynecological bleeding disorder;

Homo sapiens.

WO200296927-A2.

05-DEC-2002

29-MAY-2002; 2002WO-US017674

29-MAY-2001; 2001US-00870161.

30-NOV-2001; 2001US-0334461P. 03-MAY-2002; 2002US-00138674. 

(RIBO-) RIBOZYME PHARM INC. CHIR ) CHIRON CORP. Mcswiggen J, Pavco P, Stinchcomb D, Sandberg J; Escobedo J, Gordon G;

WPI; 2003-140439/13.

Novel enzymatic nucleic acids, ribozymes, which modulate expression of genes encoding vascular endothelial growth factor and/or VEGF receptor, useful for inhibiting tumor angiogenesis in cell, and for treating

Disclosure; SEQ ID NO 1056; 172pp; English.

cancer

The invention relates to enzymatic nucleic acids (I) i.e.

cribozymaes/Dixaymes/Chizaymes that target and modulate expression of, genes
encoding vascular endothablial growth factor (WEGP) and/or WEGP receptor
(WEGPRI and 2 encode by the Flt-1 and Kdr genes respectively). Also
(WEGPRI and 2 encode by the Flt-1 and Kdr genes respectively). Also
(T) to a call (by contacting the cell with the compound under conditions
(T) to a call (by contacting the cell with the compound and the other drug under conditions suitable for the
administration), administrating (I) to a mammal (by contacting the mammal
with the compound under conditions suitable for the
administration), administering (I) to a mammal (by contacting the mammal
with the compound under conditions suitable for the
administration), administering to subject, a nucleic acid molecule (II) that
with a subject having endometricals (by contacting the mammal
with a chemotherapeutic agent comprising contacting the mammal with the
compound and the Chemotherapeutic agent under conditions suitable for the
administration). (I) and administered to a mammalian cell, preferably
with a chemotherapeutic agent comprising contacting the mammal with the
compound and the Depending of the chemotherapeutic agent under conditions suitable for the
administration). (I) a administered to a mammalian cell, preferably
with a chemotherapeutic agent comprising contacting the mammal with the
compound and the presence of a delivery reagent which is a lipid such as
cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acids are useful for
confour vegres gene, and is in a hammal and organe, DNAzyme, G-cleaver,
or Amberzyme configuration. The enzymatic nucleic acids are useful for
treating a subject having a condition associated with an increased level
cancer (such as renal cell catinopathy, in a subject. They are also useful for
treating a subject having a condition associated with an increased level
cancer (such as renal cell catinopathy, proceeding a subject preferably paracti

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Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

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Homo sapiens
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Best Local Simi
Matches 13;
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Matches
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                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and 65% identity to (S1). A polypeptide of the invention acts as a agonist o
                                                                                                                                                           Human; 88; probe; myosin-like protein-1; hGDMLP-1; hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder; skeletal muscle function.
                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shannon MB;
                        ö
         Length 17;
                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank D,
         Score 12.4;
Pred. No. 86;
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 10029; Opp; English.
                                                                                                                                              Human GDMLP-1 probe SEQ ID NO:10029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                               ACN73127 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                     2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                             2001WO-US000665.
                                                                                                                                                                                                                                                                                                                                                             2001WO-US000669
2001WO-US000670
                                                                                                                                                                                                                                                                                                                                                                             2001US-0266860P
2001US-00866108
         16.1%;
                                                                                                                                                                                                                                              26-NOV-2003; 2003US-00723361
                                       CTCTGGAGTCCTCT 39
                                                       cucedcadeuccucu 15
                                                                                                                               (first entry)
Query Match
Best Local Similarity 64.5.
The 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu Y, Ji Y, Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-533378/51.
                                                                                                                                                                                                                                                                                                                                                                                                    GU Y.
JI Y.
PENN S G.
HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHANNON M B.
                                                                                                                                                                                                                                                                                                                                                                                                                                     RANK D.
CHEN W.
                                                                                                                                                                                                              JS2004137589-A1
                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
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30-JAN-2001; 2
30-JAN-2001; 2
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                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                               27-SEP-2000;
                                                                                                                               02-DEC-2004
                                                                                                                                                                                                                             15-JUL-2004
                                                                                                               ACN73127;
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(JIYY/)
(PENN/)
(HANZ/)
(RANK/)
(CHEN/)
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antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to novel methylation state information about CpG islands in the promoter region of a gene associated with primary liver cancer, its use and a reagent kit for detecting primary liver cancer. The reagent kit contains a methylation-specific restriction endonucless and the promoter CpG island-specific primer pairs of a gene associated with liver cancer, a reagent for transforming the methylation cytosine to uracil and primers for the promoter CpG island of the gene associated with liver cancer. The present sequence is that of a PCR primer which was for amplification of a region of a human liver cancer-associated gene promoter during the analysis of methylation state in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human liver cancer-associated gene promoter-related PCR primer SeqID107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methylation state of liver cancer related gene promoter CpG island and its use in detecting liver cancer.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                      16.1%; Score 12.4; DB 1; Length 17; 92.9%; Pred. No. 86; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                           Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
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92.9%; Pred. No. 86;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHAN-) SHANGHAI INST ONCOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
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tes 13; Conserv
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cancer,

expression. (I) is useful for treating cancer, such as pancreatic

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The invention relates to a double-stranded short interfering RNA (siRNA) molecule (I) comprising a first nucleotide sequence having 19-23 nucleotides complementary to an RNA sequence encoding HERZ or its portion, and a second nucleotide sequence having 19-23 nucleotides exhibiting complementarity to the first sequence, and including at least one nucleotide that is not a 2'-OH containing ribonucleotide. Also described is a method of producing a class of nucleic acid-based gene modulating agents that exhibit a high degree of specificity for RNA of a desired target. (I) is useful for modulating HERZ activity in a cell, and for treating diseases or conditions related to levels of HERZ gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel double-stranded short interfering RNA molecule having first nucleotide sequence complementary to RNA encoding HBR2 or its portion, and second nucleotide sequence having complementarity to first sequence,
                                                                                                                                                                                                                                                                                                                                                     short interfering RNA; siRNA; RNA interference; gene silencing;
                                                                                                                                                                                                                                                                                   Human HER2 substrate RNA sequence SEQ ID NO:5441.
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                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; cancer; HER2; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001US-0306883P.

13-AUG-2001; 2001US-0306883P.

10-SEP-2001; 2001US-031865P.

10-KEB-2002; 2001US-0318471P.

20-KAX-2002; 2002US-0358580P.

11-MAX-2002; 2002US-0363124P.

20-MAY-2002; 2002US-0363124P.

29-MAY-2002; 2002US-0365876.

29-MAY-2002; 2002US-03165876.

06-JUN-2002; 2002US-0316788.

06-JUN-2002; 2002US-0316782P.

06-JUN-2002; 2002US-031678P.

06-JUN-2002; 2002US-031678P.

06-JUN-2002; 2002US-031678P.

06-SEP-2002; 2002US-0406784P.

09-SEP-2002; 2002US-0409293P.
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                                                                        ADZ34403 standard; RNA; 17 BP
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20-FEB-2003; 2003WO-US005028.
20-FEB-2003; 2003WO-US005346.
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24-APR-2003; 2003US-00422704.
30-APR-2003; 2003US-00427160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-NOV-2003; 2003US-00724270
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                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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06-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
                bladder cancer, lung cancer, breast cancer or prostrate cancer. The present sequence represents a human HRR2 substrate RNA sequence for a DNAzyme (ribozyme), which is used in an example from the present invention for the identification of potential target sites in human HER2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antifilammatory; antiatrathritic; antiposriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; porianis; vertuca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                     Score 12.4; DB 1; Length 17; Pred. No. 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin subunit beta 3 substrate sequence SEQ ID NO:6230.
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                                                                                                                                 Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;
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                                                                                                                                                                                                              3; Mismatches
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                                                                                                                                                                       ch 16.1%;
| Similarity 71.4%;
| 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-591315/50.
                                                                                                                                                                                            Local Similarity
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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase calpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; MCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; beast cancer; Alzheimer's disease; disease; disease; bepatitis B infection; hepatocellular carcinoma; genetic drift; human;
AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit betaa, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, veruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Oslar-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit beta-3
                                                                                                                                                                                                                                                                          Gaps
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Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                      Query Match 15.8%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 92; Matches 14; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                         Sequence 17 BP; 5 A; 7 C; 2 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BACE DNAzyme substrate sequence #192.
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990S-0156236P.

990S-0156467P.

990S-0169100P.

990S-00474432.

990S-0173612P.

990S-0173612P.
                                                                                                                                                                                                                                                                                                         16 GGGGATACAACTCTGGA 32
                                                                                                                                                                                                                                                                                                                                                                                                                         ADV05926 standard; RNA; 17 BP
                                                                                                                                                                                                                                                                                                                                        GGGGTATTACTCTGGA 1
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2000US-00578223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200116312-A2.
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Karpeisky A, I
Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
20-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FBB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1999;
29-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADV05926;
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molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (FFB-1B), methionine minopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (FKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (ps-2), and hepatitis by virus (HWV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HM), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatitis B infections, and hepatitis and hepatitis and seases. Alzheimer carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present calls and to detect the presence of specific RNA in a cell. The present examples of the present invention. Note: Some SBQ ID Nos are repeated more than once in the specification, but these have different sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; halrpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; cancer; beast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; agg-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                     Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                  The present invention relates to the use of enzymatic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%; Score 12.2; Di
58.8%; Pred. No. 92;
tive 4; Mismatches
                                                                                                                          Sxample 4; Page 380; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0151713P.
99US-00406643.
99US-0156236P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCTGATGTCCTGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.8°
Best Local Similarity 58.8°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200116312-A2
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27-SEP-1999;
27-SEP-1999;
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molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (FTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (MTBRT), protein kinase C alpha (FKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), protein kinase C presentiin-2 (ps-2), and hepatitis B virus (HBN) proteins. The enzymatic nucled nammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, c include nammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, c for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as sell agiagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present encorred in the presence of sequence for a riboxyme used in the presence of sequence a riboxyme used in the control of the actions which the present the presence of sequence for a riboxyme used in the control of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                   Burgin A;
Draper K, Chowrira B;
I, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the use of enzymatic nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                               Matulic-Adamic J, Sweedler D, Dr
Beaudry A, Zinnen S, Lugwig J,
                                                                                                                                                                                                                                                                                                                                                                                   Beigelman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 371; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Blatt L,
                   99US-00436430.
99US-0169100P.
99US-00474432.
99US-0173612P.
99US-00476387.
                                                                                                                                                                                                                      2000US-0197769P
99US-0156467P
                                                                                                                                                                                            2000US-00531025
                                                                                                                                                                                                                                                                            2000US-00636385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-244406/25.
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                                                                                                                                                                                                                                                                                                                                                                                   Mcswiggen J, U
Karpeisky A, N
Stinchcomb D,
                      08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
29-DEC-1999;
30-DEC-1999;
04-FEB-2000;
                                                                                                                                                                                            20-MAR-2000;
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Gaps 10; Conservative

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||:|:|:|:|:|GCUGGCAAG 17 77 61 GCTGATGTCCTGTCAAG 쉱

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTBRT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HBR2; Human BACE G-cleaver ribozyme substrate sequence #97. ADV04194 standard; RNA; 17 BP (first entry) 10-FEB-2005 ADV04194; 

hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amborzyme; zinzyme; Oacer; breadt cancer; Alzheimer's disease; diabetes; obseity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; 99US-00406643. 99US-0156236P. 99US-0156467P. 99US-00436430. 99US-00474432. 99US-0047612P. 99US-00476387. 20-MAR-2000; 2000US-00531025. 14-APR-2000; 2000US-0197769P. 23-MAY-2000; 2000US-00578223. 2000WO-US023998 2000US-00636385 WO200116312-A2. Homo sapiens. 30-AUG-2000; 09-AUG-2000; 30-DEC-1999; 04-FEB-2000; 29-DEC-1999 08-MAR-2001 31-AUG-1999 27-SEP-1999 27-SEP-1999 08-NOV-1999 06-DEC-1999 

Chowrira B; Matulic-Adamic J, Sweedler D, Draper K, Ch Beaudry A, Zinnen S, Lugwig J, Sproat BS, Burgin A; Beigelman L, Burg.... Draper K, Usman N, Blatt L, Stinchcomb D, Mcswiggen J, Karpeisky A,

(RIBO-) RIBOZYME PHARM INC.

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes obesity and heart disease.

Example 4; Page 366; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERA/C-erb2/neu), phospholamban (PLM), presentin-1 (ps-1), presentin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (incyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Albriemer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, agg-related diseases, hepatitis B infections, and hepatitis and hepatocellular cardimomar. The enzymatic nucleic acid molecules can also be used as setting and to detect the presence of specific RNA in a cell. The present cancer in particular breast engine arriboryme used in the content of the presence of specific RNA in a cell. The present cancer in the present cancer in a ribozyme used in the present cancer in t E the present invention. Note: Some SEQ ID Nos are repeated in the specification, but these have different sequences associated with them. the examples of more than

Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;

Gaps ; 0 15.8%; Score 12.2; DB 1; Length 17; 58.8%; Pred. No. 92; ive 4; Mismatches 3; Indels Local Similarity 58.8 es 10; Conservative Query Match Matches

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61 GCTGATGTCCTGTCAAG 77 ð

1 GCUGGUGCUGCCAAG 17

ADV06876 standard; RNA; 17 BP

ADV06876;

(first entry) 10-PEB-2005

Human BACE amberzyme ribozyme substrate sequence #97.

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; disease; besity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

Homo sapiens

#0200116312-A2.

08-MAR-2001.

30-AUG-2000; 2000WO-US023998

990S-00406643. 990S-0156236P. 990S-00436467P. 990S-0169100P. 990S-017361432. 990S-01736142. 27-SEP-1999

27-SEP-1999; 99US-0156467P.
08-NOV-1999; 99US-0156467P.
29-DEC-1999; 99US-00474432.
29-DEC-1999; 99US-00474432.
30-DEC-1999; 99US-00476387.
04-FRB-2000; 2000US-00531025.
14-APR-2000; 2000US-00531025.

2000US-00636385 09-AUG-2000;

(RIBO-) RIBOZYME PHARM INC.

Chowrira Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Ch Beaudry A, Zinnen S, Lugwig J, Sproat BS; Mcswiggen J, Ul Karpeisky A, Ma Stinchcomb D, 1

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WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes. obesity and heart disease.

Example 4; Page 391; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBR), protein kinase C alpha (FRC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presentiln-1 (ps-1), presentiln-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HB), hairpin, NCT (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful

for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac disease e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepaticis and becocellular cardinomar. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for a ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them. 888888888888888

Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;

Gaps .. 0 DB 1; Length 17; 3; Indels 15.8%; Score 12.2; E 58.8%; Pred. No. 92; tive 4; Mismatches Local Similarity 58.8 Query Match fatches

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77 61 GCTGATGTCCTGTCAAG

8 셤

17 GCUGGUGUGCUGGCAAG

RESULT

ACN05922 standard; RNA; 17

ВР

ACN05922;

22-APR-2004 (first entry)

WNV Amberzyme substrate SEQ ID NO 5925.

WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic; viruolė; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme; 

Amberzyme; Zinzyme; ss

West Nile Virus.

WO200268637-A2.

06-SEP-2002.

19-OCT-2001; 2001WO-US048350.

20-OCT-2000; 2000US-0242411P.

(RIBO-) RIBOZYME PHARM INC

(BLAT/) BLATT L. (MCSW/) MCSWIGGEN J A.

Mcswiggen JA; Blatt L,

WPI; 2002-706994/76.

New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 23; SEQ ID NO 5925; 495pp; English.

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (RNV). The nucleic acid molecules are useful for treating a condition related to WVV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least that 2-O-methyl moddifications, phosphorothicate linkages on at least three of the 5' terminal nucleocides and a 3' and modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

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82.4%; Pred. No.

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15.8%; Score 12.2; DB 1; Length 17;
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Query Match

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are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                  DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WNV minus strand Inozyme substrate SEQ ID NO 11562.
                                                                                                                                                                    Sequence 17 BP; 6 A; 2 C; 8 G; 0 T; 1 U; 0 Other;
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                                                                                                                                                                                                                                              Query Match 15.8%; Score 12.2; D
Best Local Similarity 76.5%; Pred. No. 92;
Matches 13; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGGCCUGGGGAAAGA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACN11559 standard; RNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                          8 GACGGCCTGGGGATACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amberzyme; Zinzyme; ss
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(MCSW/) MCSWIGGEN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-706994/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200268637-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN11559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; restenceis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; seppis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                d-cleaver; amberzyme cancer; REL-A activity; breast cancer; human; cesophageal cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; cervical cancer; pancreatic cancer; cervical cancer; pancreatic cancer; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; pacliteat; docterate; rapplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
                                                                                                                                                                                                                                                                                                                                                                   Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
                       Gaps
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                       Indels
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                     Mismatches
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                                                                                                                                                                                                     ACA09006 standard; RNA; 17 BP
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94US-00245466.
94US-00291932.
96US-00777916.
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                                                                                                  17 GAAGGCCTGGGGAAAGA 1
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                                                             8 GACGGCCTGGGGATACA
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Best Local Similarity 82.4
Matches 14; Conservative
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15-AUG-1994;
23-DEC-1996;
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cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoria arthritis, restencisis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocarchial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ4; MDZ4; MDZ1; hDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MDZ3 scanning oligonucleotide SEQ ID 310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%; Score 12.2; I
82.4%; Pred. No. 92;
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AAGACGCCTGGGGATA
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nes 14; Conservative
                                                                                                                                                                                                                                                                                                                           nucleic acid molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; ss.
                                                                                                                                                                                                                                                                                                                                                             Murine oligonucleotide associated with tumour supression, SEQ ID 5066.
                                                                                                                Gaps
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proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specifically cancer but also Alzheimer's disease and schizophrenia
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                                                                                DB 1; Length 17;
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                                                Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
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                                                                               15.8%; Score 12.2; D
82.4%; Pred. No. 92;
tive 0; Mismatches
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Pred. No. 92;
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                                                                                                                                                28 CTGGAGTCCTCTGAGAG 44
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Local Similarity 82.4%;
hes 14; Conservative
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                                                                                               Local Similarity 82.4
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   proteins are useful
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                                                                                Query Match
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diabetic retinopathy; age related macular degeneration; and disorder; rheumatoid arthritis; psoriasis; wound healing; and angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing; endometriosis; endometroid carcinoms; gynecological bleeding disorder; menstruation disorder; premenstrual syndrome; menopause; Gynecological; Cytoseratic; Ophthalmological; Antidiabetic; antiangiogenic; Antirheumatic; Antitheumatic; Antitheumatic; Antiarthritic; Vulnerary; Hemostatic; Contraceptive; 8s; enzymatic nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel enzymatic nucleic acids, ribozymes, which modulate expression of genes encoding vascular endothelial growth factor and/or VEGF receptor, useful for inhibiting tumor angiogenesis in cell, and for treating
                                                                                                   Human VEGF receptor 21 (Kdr) DNAzyme target sequence SEQ ID 4058.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Escobedo J, Mcswiggen J, Pavco P, Stinchcomb D, Sandberg J;
                                                                                                                             receptor; angiogenesis; cancer; tumor; ocular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 4058; 172pp; English.
                           AEB61480 standard; mRNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                           29-MAY-2001; 2001US-00870161.
30-NOV-2001; 2001US-0334461P.
03-MAY-2002; 2002US-00138674.
                                                                                                                                                                                                                                                                                                                   29-MAY-2002; 2002WO-US017674.
                                                                                                                                                                                                                                                                                                                                                                                              (RIBO-) RIBOZYME PHARM INC.
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-140439/13
                                                                                                                                                                                                                                                                   WO200296927-A2.
                                                                                                                                                                                                                                            Ношо варіелв
                                                                           22-SEP-2005
                                                                                                                                                                                                                                                                                            05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon G;
                                                     AEB61480;
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The invention relates to enzymatic nucleic acids (I) i.e.
ribozymes/DNAzymes/Zinzymes that target and modulate expression of, genes
croribozymes/DNAzymes/Zinzymes that target and modulate expression of, genes
croribozymes/DNAzymes/Zinzymes that that the and/or VEGF receptor
(VEGFR1 and 2 encode by the FIt-1 and Kdr genes respectively). Also
croribozymes/DNAzymes/Electrical and carrier, administering
croribozymes/DNAzymes/Electrical and carrier, administering
croribozymes/DNAzymes/Electrical and carrier, administering
conjunction with one or more other drug by contacting the cell with the
compound and the other drug under conditions suitable for the
administration), administering (I) to a mammal (by contacting the mammal
crowith the compound under conditions suitable for the
administration) administering endometricois (by contacting the mammal
crowith, or administering to subject, a nucleic acid molecule (II) that
modulates expression of VEGF, VEGFRI, and/or VEGFR2), a mammalian cell
crompound and the chemotherapeutic agent under conditions suitable for the
modulates expression of VEGF, VEGFRI, and/or VEGFR2), a mammal with the
compound and the chemotherapeutic agent under conditions suitable for the
compound and the chemotherapeutic agent under conditions suitable for the
compound and the chemotherapeutic agent under conditions suitably to
human cell in the presence of a delivery reagent which is a lipid such as
cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acid
molecule has an endonuclease activity to cleave RNA encoded by an VEGFR2
and/or VEGFR2 gene, and is in a hammerhead, inozyme, DNAzyme, G-cleaver,
cor Amberzyme configuration. The enzymatic nucleic acid molecule has an endonuclease activity to cleave RNA encoded by an VEGFR2
and/or VEGFR2 gene, and is in a hammerhead, inozyme, DNAzyme, G-cleaver,
cor Amberzyme configuration. The enzymatic nucleic acid
inhibiting subject having a condition associated with an increased level
cromible of the proposed of the proposed of the proposed of

of VEGF receptor, where the condition is cancer, e.g. breast cancer, lung cancer (such as non-small cell lung carcinoma), colorectal cancer, renal cancer (such as non-small cell carcinoma), pancreatic cancer. The enzymatic nucleac acids are useful for treating a subject (preferably human) having endometriosis, psoriasis, age-related macular degeneration, proliferative diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis, wound healing, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome, and emopausal dysfunction. The enzymatic nucleic acids are useful for birth control by inhibiting ovulation or embryonic uterine implantation. The present sequence is a target sequence from the human VEGFR2/Kdr mRNA. 888888888888888

Sequence 17 BP; 7 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

Gaps ô Query Match 15.8%; Score 12.2; DB 1; Length 17; Best Local Similarity 82.4%; Pred. No. 92; Matches 14; Conservative 0; Mismatches 3; Indels

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RESULT 93

DNA detection extension primer #36. 멾. ADX84037 standard; DNA; 17 05-MAY-2005 (first entry) ADX84037; ADX84037

Analysis; mass spectroscopy; PCR; primer; ss. WO2005014850-A2 17-FEB-2005 Synthetic.

06-AUG-2004; 2004WO-US025526 06-AUG-2003; 2003US-0493238P. CCCCCCCCCCCCX8X4444X8X1X8X8X8X8X8X8X8X8X8X8X8X

(UYMA-) UNIV MASSACHUSETTS.

Galdzicka M;

Ginns EI,

WPI; 2005-195764/20.

Clinical assay system for assaying sample, has central controller, sample transfer module, nucleic acid extraction and measurement module, thermocycling module, primer extension module, mass spectrometry module analyzing sample.

Claim 6; SEQ ID NO 108; 207pp; English

The invention relates to a system for performing an assay on a biological sample, comprising a central controller programmed to exchange information about the biological sample with an outside system or database and exchange information about the biological sample with one or more modules of the system, a sample transfer module for transferring a portion of the sample to a first container, a nucleic acid extraction and for transferring the portion from the first container to a second container, a nucleic acid measurement module for measuring the portion and for transferring the portion from the first container to a second container, a nucleic acid measurement module for measuring the concentration of nucleic acids in the portion, a the portion module for adding PCR reaction materials to the portion, a thermocycling module for amplifying a target sequence and extending a primer in the portion, a primer extension preparation module for adding primer extension reaction materials to the portion, a mass spectrometry preparation module for

RESULT 95 ADR 70044

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removing a sample of the portion from the second container to a support for analysis by mass spectrometry and a mass spectrometry module for analyzing the sample. The invention also relates to an automated method for detecting mutations in a target gene. The diagnostic assay is an assay for detecting a pathogen in the sample. The pathogen is a virus, bacterium or fungus. The virus is a virus of the family Herpesviridae, preferably Cytomegalovirus (CMV). The system enables high accurate assays on nucleic acid sequences (e.g. clinically relevant nucleic acid sequences) using mass spectrometry. This sequence represents a DNA detection extension primer used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises the amino acid and coding sequences of SLC26A6, SLC26A1 and SLC26A2 anion transporter proteins. The DNA and protein sequences of the invention are useful for treating cancer. The present DNA sequence represents a splice site from the gene encoding the mouse SLC26A6 anion transporter protein.
                                                                                                                                                                                                                                                                 Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New SLC26A6, SLC26A1 or SLC26A2 polypeptide, useful for preparing composition for treating e.g., cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse SLC26A6 anion transporter protein gene splice site #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;
                                                                                                                                                                                                                             DB 1; Length 17;
                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                         Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                           Pred. No. 92;
                                                                                                                                                                                                                           15.8%; Score 12.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 37; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVA-) UNIV VANDERBILT.
(UYCA-) UNIV CASE WESTERN RESERVE.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
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                                                                                                                                                                                                                    Query Match 15.00,
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                               25 ACTCTGGAGTCCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                   ADM56305 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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ss; antianglogenic; cytostatic; antiarteriosclerotic; antipsoriatic; antidabetic; ophthalmological; antiarthritic; antirheumatic; antiallergic; antinflammatory; dermetological; anti-HIV; virucide; survivin antagonist; apoptosis inhibitor; callular proliferation inhibitor; survivin; gene expression; abnormal angiogenesis; chemotherapeutic agent; busulfan; myleran; carboplatin; paraplatin; Taxol; doxorubicin; adriamycin; atherosclerosis; psoriasis; diabetic retinopathy; rheumacoid arthritis; asthma; warts; allergic dermatitis; cancer; tumour; sarcoma; glioma; carcinoma; melanoma; osteosarcoma; Bwing's sarcoma; chondrosarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an oligomeric compound (1) capable of modulating survivin expression, having 8-50 nucleotides and/or nucleotide analogues, where the compound comprises a subsequence of at least 8 nucleotides or nucleotide analogues, where the subsequence is located within a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New locked nucleic acid containing oligomeric compound capable of modulating survivin expression, useful for treating cancer such as breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,'5
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "OTHER = phosphorothioate internucleotide
linkages, all locked nucleic acid (LNA) residues are
methyl cytosine residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "OTHER = beta-D-oxy-locked nucleic acid but
optionally DNA nucleotides, optionally phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "OTHER = beta-D-oxy-locked nucleic acid but optionally DNA nucleotides, optionally phosphate internucleotide linkages"
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                                                                                            Human survivin gene modulatory oligonucleotide #112.
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                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma, lung carcinoma, etc.
 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2004; 2004WO-DK000096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-FBB-2003; 2003DK-00000183
18-NOV-2003; 2003DK-00001708
ADR70044 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANT-) SANTARIS PHARMA AS.
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
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                                                                                                                                                                                                                                                                                                 Paclitaxel, Docetaxel.
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modified_base
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                                                             04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                              Synthetic.
                             ADR70044;
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Gaps

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0; Indels

15.6%; Score 12; DB 1; Length 12;

100.0%; Pred. No. 67; ive 0; Mismatches

12; Conservative GACGGCCTGGGG 19 GACGGCCTGGGG 1

8 12

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Best Local Similarity

Query Match Matches

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chosen from one of 143 sequences given in the specification. (I) is useful for treating a mammal suffering from or susceptible from a disease caused by abnormal anglogenesis, by administering (I) containing one or more LNA units that are targeted to survivin. (I) is useful as a medicament and for the manufacture of a medicament for the treatment of cancer, in combination with chemotherapeutic agent such as busulfan (myleran), carboplatin (paraplatin), Taxol, doxorubicin (adriamycin), etc. (I) or a conjugate (II) containing (I) is useful in the preparation of a medicament for the treatment of atherosclerosis, psoriasis, diabetic carcinomant for the treatment of atherosclerosis, psoriasis, diabetic carcinoma of a solid tumour, sarcoma, glioma or carcinoma chosen from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast carcinoma, non-small cell lung cancer, strong carcinoma, bandcer carcinoma, ovariant carcinoma, prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid automous. The malignant melanoma is colorectal melanoma, and languatic melanoma, lentigo malignant melanoma, accinoma, and malignant melanoma, accinoma, accino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma; basal cell carcinoma; ovary tumor; breast tumor; broadcartumor; non-small-cell lung cancer; renal cell carcinoma; bladder tumor; mon-small-cell lung cancer; pancreas tumor; lung tumor; uterine cervix tumor; carcier; pancreas tumor; lung tumor; colorectal tumor; we arcoma; osteosarcoma; Kaposis sarcoma; anti-HIV; glioma; cytostatic; monocrine disease; gynecology and obstetrics; genitourinary disease; respiratory disease; musculoskeletal disease; dermatological disease; proliferative disorder; atherosclerosis; antiarteriosclerotic; cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic; ardiovascular disease; coular disease; rheumatoid arthritis; antisevantic; inflammation; asthma; antiasthmatic; antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic; verruca vulgaris; virucide; cell proliferation; apoptosis modulation; angiogenesis disorder; survivin; phosphorothioate; cytosine methylation; antisense oligonucleotide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma, chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's sarcoma. The treatment further involves administration of a chemotherapeutic agent such as taxanes, preferably Taxol, Paclitaxel or Docetaxel. (I), (II) or (III) is also useful for preventing or limiting apoptosis or for preventing cellular proliferation. This sequence corresponds to an antisense oligonucleotide targeted to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.6%; Scor.
100.0%; Pred. No. 2...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 CCAGCGAAGCTG 64
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Location/Qualifiers

Homo sapiens

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1. .16 /\*tag=

misc\_binding

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The invention relates to antibense originalities consisting or s-30 mucleotides and/or nucleotide analogs which inhibit expression of human survivin, an inhibitor of apoptosis which is also essential for cell division and angiogenesis. The antisense oligonucleotides comprise a subsequence of 8 or more nucleotides or nucleotide analogs, wherein the subsequence is located within a sequence selected from ADW0944-ADW09586. The oligonucleotides preferably contain one or more (preferably 6-10) nucleotide analogs, especially a locked nucleic acid (LNA), and also preferably contain a linkage group selected from a phosphate group, a phosphorothicate group or a boranophosphate group, and also crelates to a conjugate comprising a survivin antisense oligonucleotide of the invention and one or more non-nucleotide, and a pharmaceutical composition comprising a survivin antisense oligonucleotide or conjugate of the invention, optionally further comprising a chemotherapeutic agent. The survivin antisense oligonucleotide, and compositions containing them, are useful in the treatment of cancers such as carcinoma, breast carcinoma, heast carcinoma, basal cell carcinoma, bandder carcinoma, non-small cell lung cancer, renal carcinoma, particular carcinoma, recurrent superficial bladder cancinoma, cervical dysplasia, larryngaal carcinoma, carcinoma, cervical carcinoma, ecricoma, cervical carcinoma, ecricoma, cervical carcinoma, eliponucleotides are also useful cumors); asrcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma, cumors); asrcomas (e.g., osteosarcoma, Ewing's sarcoma, conditions such as atherosclerosis, psoriasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts, and allergic certinopathy theumatoid arthritis, asthma, warts, and allergic certinopathy they may additionally be used for inhibiting cellular certinopathy they may additionally be used for inhibiting cellular cellular paperation, for modulating apportoria arthrisms allegence of securical such as a securical angiosence of securical such as a secur
                                                                                                                                                                         /mod_base= OTHER
/mod= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D
-oxy-LNA cytosines are 5-methylcytosine"
13. .16
                                                                                                                                                                                                                                                                                                 /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are 5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligomeric compound for the modulation of survivin, useful for treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts, or allergic dermatitis.
/bound moiety= "Bases 1568-1553 of human survivin cDNA (SEQ 1D NO:1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense oligonucleotides consisting of 8-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Westergaard M, Petersen KD, Wissenbach M;
                                                                                                             /note= "Phosphorothioate linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 10; SEQ ID NO 592; 264pp; English.
                                                                                         /mod_base= OTHER
                                                                                                                                                                                                                                                                                    OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-2004; 2004US-00776934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-2003; 2003US-0446372P
19-NOV-2003; 2003US-0523591P
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/*tag= a
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(WEST/) WESTERGAARD M.
(PETE/) PETERSEN K D.
(WISS/) WISSENBACH M.
                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                      mod/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-100663/11.
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                                                 modified base
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Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma; basal cell carcinoma; ovary tumor; breast tumor; breast tumor; cancer; pancreas tumor; prostatic cancer; pancreas tumor; lung tumor; atomach tumor; prostatic cancer; pancreas tumor; lung tumor; cervical dysplasia; colon tumor; colorectal tumor; arcoma; osteosarcoma; kaposis sarcoma; anti-HIV; glioma; cytostatic; andocrine disease; grancology and Obstetrics; genitourinary disease; weapfratory disease; metabolic disease; dermatological disease; respiratory disease; metabolic disorder; psoriasis; antipsoriatic; cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic; ardiovascular disease; ocular disease; rhematological; antiathritic; antirheumatic; inflammation; asthma; antiasthmatic; skin allery; antiallergic; antiinflammatory; dermatological; vertuce vulgaris; virucide; cell proliferation; apoptosis modulation; antisense oligonucleotide; se.
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All beta-D-oxy-LNA cytosines are 5-methylcytosine"
of the invention are shorter than prior art survivin antisense oligonucleotides (16-mers compared to 20-25-mers), therefore having increased specificity and affinity for survivin mRNA, and also have higher biostability and cell permeability. The present sequence represents an antisense oligonucleotide targeted to the human survivin cDNA target sequence shown in ADW09443 used in an example of the
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                                                                                                                                                               DB 1; Length 16; 92;
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'note= "Phosphorothioate linkages"
                                                                                                                                Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                               0; Mismatches
                                                                                                                                                               Score 12;
Pred. No.
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                                                                                                  invention
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/note= "Optionally beta-D-oxy-LNAB. All beta-D-oxy-LNA cytosines are 5-methylcytosine. Optionally phosphorothioate linkages when bases 13-15 are beta-D-oxy-LNAB. When nucleotides 13-15 are unmodified, the internucleotide linkages are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                         /note= "Optionally beta-D-oxy-LNA. When this nucleotide is unmodified, the linkage between nucleotides 15 and 16 is phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts, or allergic dermatitis.
                                                                                                                                                                                            /mod_base= OTHER // phosphorothioate linkage when force= "Optionally phosphorothioate linkage is nucleoide 16 is beta-D-oxy-LWA. This linkage is phosphorothioate when nucleotide 16 is unmodified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Westergaard M, Petersen KD, Wissenbach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligomeric compound for the modulation of survivin, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 113; 264pp; English.
                                                                                                                                                                                                                                                                                                                                           /*tag= g
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-PEB-2004; 2004US-00776934.
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WESTERGAARD M.
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WISSENBACH M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-100663/11.
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                                                                                                                                         modified base
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The invention relates to antisense oligonuclectides consisting of 8-50 nuclectides and/or nuclectide analogs which inhibit expression of human survivin, an inhibitor of apoptosis which is also essential for cell division and angiogenesis. The antisense oligonuclectides comprise a subsequence of 8 or more nuclectides or nuclectide analogs, wherein the subsequence of 8 or more nuclectides or nuclectide analogs, wherein the subsequence of 8 or more nuclectides or nuclectide analogs, wherein the subsequence of 8 or more nuclectides or nuclectide analogs, specially a locked nucleic acid (LNA), and also preferably contain a linkage group selected from a phosphate group, a phosphorothicate group or a boranophosphate group. The invention also cor or nuclectide or non-polymuclectide of the invention and one or more non-nuclectide or non-polymuclectide of the invention and one or more non-nuclectide or non-polymuclectide of composition and one or more non-nuclectide or non-polymuclectide of the invention and one or more non-nuclectide or non-polymuclectide of coft the invention and one or more non-nuclectide or non-polymuclectide or composition and one or more non-nuclectide or non-polymuclectide or conjugate of of the invention and one or more non-nuclectide or non-polymuclectide or conjugate of extension, are useful in the treatment of cancinoma, breast carcinoma, breast carcinoma, breast carcinoma, non-small cell lung cancer, renal cell carcinoma, cervical darcinoma, non-small cell lung cancer, renal cell carcinoma, cervical carcinoma, pancreatic carcinoma, cervical carcinoma, cervical darcinoma, cervical darcinoma, cervical serection pancreal carcinoma, cervical carcinoma, cervical serection pancreal carcinoma, cervical carcinoma, cervical carcinoma, sud Kaposi's sarcoma); or gliomas. The survivin antiense oligonuclectides are also useful in the retinopathy, rheumatoid arthritis, asthma, warts, and allergic dermatitis. They may additionally be used for inhibiting cellular cerimon, for modulating apoptosis and for tre

/mod base= OTHER

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Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma; basal cell carcinoma; ovary tumor; breast tumor;

non-small-cell lung cancer; renal cell carcinoma; bladder tumor;

mon-small-cell lung cancer; pancreas tumor; lung tumor;

uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;

sarcoma; osteosarcoma; Kaposis sarcoma; anti-HIV; glioma; cytostatic;

medocrine disease; gynecology and obstetrics; genitourinary disease;

respiratory disease; musculoskeletal disease; dermatological disease;

metapiratory disease; metabolic disorder; psoriasis; antipsoriatic;

tmmune disorder; diabetic retinopathy; antidiabetic; ophthalmological;

mentiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;

skin allergy; antiallergic; antiinflammatory; dermatological;

verruca vulgaris; virucide; cell proliferation; apoptosis modulation;

manisquenesis disorder; survivin; phosphorothioate; cytosine methylation;

mutisense oligonucleotide; se.
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   to abnormal angiogenesis. The survivin antisense oligonucleotides
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related to abnormal angiogenesis. The survivin antisense oligonucleotide of the invention are shorter than prior art survivin antisense oligonucleotides (16-mers compared to 20-25-mers), therefore having increased specificity and affinity for survivin mRNA, and also have higher blosteablity and cell permeability. The present sequence represents a specifically claimed antisense oligonucleotide targeted to the human survivin cDNA target sequence shown in ADW09443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /bound moiety= "Bases 1568-1553 of human survivin cDNA (SEQ 1D NO:1)"
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human survivin antisense oligonucleotide 113B, SEQ ID NO:593.
                                                                                                                                                                       Score 12; DB 1; Length 16;
Pred. No. 92;
                                                                                                                                                                                                        0; Indels
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/note= "Phosphorothioate linkages"
                                                                                                                                       Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
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100.0%; Pred. No.
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                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                         CCAGCGAAGCTG 15
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The invention relates to antisense oligonuclectides consisting of 8-50 aurolectides and/or nuclectide analogs which inhibit expression of human survivin, an inhibitor of apoptosis which inhibit expression of human survivin, an inhibitor of apoptosis which inhibit essential for cell division and anglogenesis. The antisense oligonuclectides comprise a ubsequence of 8 or more nuclectides or nucleotides analogs, wherein the subsequence is located within a sequence selected from ADW0944-ADW09586. The oligonucleotide analogs, especially a locked nucleic acid (LMA), and also preferably contain a linkage group selected from a phosphate group, a preferably contain a linkage group selected from a phosphate group, a preferably contain a linkage group selected from a phosphate group, a preferably contain and one or more non-nucleotide or conjugate comprising a survivin antisense oligonucleotide and a pharmaceutical composition comprising a survivin antisense oligonucleotide and a pharmaceutical composition comprising a survivin antisense oligonucleotide, and a pharmaceutical containing them, are useful in the treatment of cancers such as carcinoma, breast carcinoma, beast calcinoma, beast carcinoma, beast calcinoma, bradder carcinoma, passal cell carcinoma, lung cancer, renal cell carcinoma, prostatic carcinoma, passal cell carcinoma, lung carcinoma, prostatic carcinoma, passal cell carcinoma, lung carcinoma, prostatic carcinoma, and kaposi's sarcoma) on sension carcinoma, prostatic carcinoma, and kaposi's sarcoma) on sension carcinoma, prostatic carcinoma, and kaposi's sarcoma) on sension carcinoma, prostatic carcinoma, and carcinoma, prostatic carcinoma, and carcinoma, cervical carcinoma, prostatic carcinoma, and carcinoma, cervical carcinoma, prostatic carcinoma, and carcinoma, prostatic carcinoma, and carcinoma, prostatic carcinoma, and carcinoma, cervical dappacelerosis, psociasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts, and allergic carcinoma are shorter than prostatic carcinoma and selected to abn
                                                                                                                                                                                                                                                                                                                                       treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts, or allergic dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        higher biostability and cell permeability. The present sequence represents an antisense oligonucleotide targeted to the human survivin cDNA target sequence shown in ADW09443 used in an example of the
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                                                                                                                                                                                                                                                                                                                      New oligomeric compound for the modulation of survivin, useful for
                                                                                                                                                                                                                                  Wissenbach M;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; SEQ ID NO 593; 264pp; English.
                                                                                                                                                                                                                                  Westergaard M,
10-FEB-2004; 2004US-00776934.
                                       10-FEB-2003; 2003US-0446372P.
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                                                                                                                           THRUE C A.
WESTERGAARD M.
                                                                                                                                                                    PETERSEN K D.
WISSENBACH M.
                                                                                                                                                                                                                                    Thrue CA,
                                                                                                                                                                                                                                                                            WPI; 2005-100663/11.
                                                                                                         HANSEN B.
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Matches
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RESULT 99 ADW10037

ADW10037 standard; DNA; 16 BP

ADW10037;

(first entry) 07-APR-2005 Human survivin antisense oligonucleotide 113D, SEQ ID NO:595.

Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma; basal cell carcinoma; ovary tumor; breast tumor;

non-small-cell lung cancer; renal cell carcinoma; bladder tumor;

non-small-cell lung cancer; renal cell carcinoma; bladder tumor;

tormach tumor; prostatic cancer; pancreas tumor; lung tumor;

tormach tumor; cervical dysplasia; colon tumor; colorectal tumor;

w arcoma; osteosarcoma; Kaposis sarcoma; anti-HIV; glioma; cytostatic;

m ancorine disease; gynecology and obstetrics; genitourinary disease;

respiratory disease; musculoskeletal disease; dermatological disease;

respiratory disease; metabolic disorder; psoriasis; antipsoriatic;

cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;

immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;

antiatrhritic; antitheumatic; inflammation; asthma; antisthmatic;

skin allergy; antiallergic; antidiflammatory; dermatological;

w verruca vulgaris; virucide; cell proliferation; apoptosis modulation;

mantisense oligonucleotide; ss.

fomo sapiens

/note= "Phosphorothioate linkages" Location/Qualifiers base= OTHER \*tag= /mod modified\_base misc\_binding

US2005014712-A1.

20-JAN-2005.

10-FEB-2004; 2004US-00776934.

10-PEB-2003; 2003US-0446372P. 19-NOV-2003; 2003US-0523591P.

HANSEN B. HANS/)

THRUB C A.
WESTERGAARD M.
PETERSEN K D.
WISSENBACH M. (THRU/)

(MISS/) PETE/

Wissenbach M; Thrue CA, Westergaard M, Petersen KD, WPI; 2005-100663/11 Hansen B,

New oligomeric compound for the modulation of survivin, useful for treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy, rheumatoid arthritis, asthma, warts, or allergic dermatitis.

Example 10; SEQ ID NO 595; 264pp; English.

The invention relates to antisense oligonucleotides consisting of 8-50 nucleotides and/or nucleotide analogs which inhibit expression of human survivin, an inhibitor of apoptosis which is also essential for cell division and anglogenesis. The antisense oligonucleotides comprise subsequence of 8 or more nucleotides or nucleotide analogs, wherein the subsequence is located within a sequence selected from ADW09444-ADW09586. The oligonucleotides preferably contain one or more (preferably 6-10) nucleotide analogs, especially a locked nucleic acid (LNA), and also preferably contain a linkage group selected from a phosphate group, a phosphorothioate group or a boranophosphate group. The invention also

cc relates to a conjugate comprising a survivin antisense oligonucleotide of the invention and one or more non-nucleotide or non-polymucleotide composition and one or more non-nucleotide or non-polymucleotide or conjugate composition comprising a survivin antisense oligonucleotide or conjugate of the invention, optionally further comprising a chemotherapeutic agent. The survivin antisense oligonucleotide or conjugate containing them, are useful in the treatment of cancers such as carcinoma, braset carcinoma, non-small call lung cancer, renal cell carcinoma, passet carcinoma, non-small call lung cancer, renal cell carcinoma, passet carcinoma, cervical carcinoma, cervical carcinoma, cervical carcinoma, cervical dysplasia, laryngeal carcinoma, carcinoma, cervical carcinoma, cervical dysplasia, laryngeal carcinoma, cervical carcinoma, fibrosarcoma, consense olgonucleotides (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma, guinomas, The survivin antisense oligonucleotides (e.g., osteosarcoma, survivin antisense oligonucleotides (fe-mers compared to 20-25-mers), therefore having criates oligonucleotides (fe-mers compared to 20-25-mers), therefore having criates entents an antisense oligonucleotide targeted to abnormal analysements an antisense oligonucleotide targeted in an example of the invention are shorter than prior at survivin antisense compared to compare invention 

Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Gaps ö Query Match 15.6%; Score 12; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 92; Matches 12; Conservative 0; Mismatches 0; Indels

ö

ð 셤 RESULT 100

ADW10036 standard; DNA; 16 BP.

ADW10036;

07-APR-2005 (first entry)

Human survivin antisense oligonucleotide 113C, SEQ ID NO:594.

Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma; basal cell carcinoma; ovary tumor; breast tumor; manal-cell lung cancer; renal cell carcinoma; bladder tumor; mon-small-cell lung cancer; renal cell carcinoma; bladder tumor; moract tumor; cervical dysplasia; colon tumor; colorectal tumor; attender cervical dysplasia; colon tumor; colorectal tumor; sarcoma; sateomarcoma; Kaposis sarcoma; anti-HIV; glioma; cytostatic; architectary disease; musculoskaletal disease; dermatological disease; proliferative disorder; atherosclerosis; antiarteriosclerotic; manual disorder; diabetic retinopathy; antidiabetic; ophthalmological; cardiovascular disease; retinopathy; antidiabetic; antifrenumatic); antidiabetic; inflammation; asthma; antiasthmatic; antifrenumatic; inflammation; asthma; antidathmatic; wertner avulgaris; virucide; cell proliferation; asthma; antidathmatic; antifrenumatic; inflammatory; dermatological; vernuca vulgaris; virucide; cell proliferation; apoptosis modulation; antidosnesis disorder; gurvivin; phosphorothioate; cytosine methylation; antisense oligonucleotide, ss.

Homo sapiens

Location/Qualifiers Д /\*tag= misc binding

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The invention relates to antisense oligonucleotides consisting of 8-50 nucleotides and/or nucleotide analogs which is also essential for cell division and inhibitor of apoptosis which is also essential for cell division and angiogenesis. The antisense oligonucleotides comprise a subsequence of 8 or more nucleotides or nucleotide analogs, wherein the subsequence is located within a sequence selected from ADW09444-ADW09586. The oligonucleotides preferably contain a linkage group selected from a phosphate group, a phosphorothioate group or a boranophosphate group. The invention also correlates to a conjugate comprising a survivin antisense oligonucleotide of the invention and one or more non-nucleotide, and a pharmaceutical composition comprising a survivin antisense oligonucleotide, and a pharmaceutical composition comprising a survivin antisense oligonucleotide, and a pharmaceutical composition comprising a survivin antisense oligonucleotide, and a pharmaceutical corrinoma, breast carcinoma, non-small cell lung cancer, renal cell carcinoma, breast carcinoma, newall call lung cancer, renal cell carcinoma, breast carcinoma, recurrent superficial bladder cancer, stomach carcinoma, recurrent superficial bladder cancer, stomach carcinoma, recurrent superficial arcinoma, lung carcinoma, prostatic carcinoma, recurrent superficial bladder cancer, stomach carcinoma, recurrent superficial arcinoma, lung carcinoma, prostatic carcinoma, recurrent superficial arrinoma, lung carcinoma, prostatic carcinoma, recurrent superficial bladder cancer, stomach carcinoma, recurrent superficial arrinoma and arcinoma, curical carcinoma, servical carcinoma, servical carcinoma, servical carcinoma, servical carcinoma, servical
                                                                                 *tag= a
/*mod_base= OTHER
/mode= "Beta-D-oxy-LNAB (locked nucleic acid). All beta-D
                                                                                                                                                                                                                                                                                                 /note= "Beta-D-oxy-LNAB. All beta-D-oxy-LNA cytosines are
5-methylcytosine"
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/bound_moiety= "Bases 1568-1553 of human survivin cDNA (SEQ \overline{\text{LD}} NO:1)"
                                                                                                                                        -oxy-LNA cytosines are 5-methylcytosine
                                                                                                                                                                                                   /mod_base= OTHER
/note= "Phosphorothioate linkages"
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                                                                                                                                                                                                                                                                                    base- OTHER
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19-NOV-2003; 2003US-0523591P.
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WESTERGAARD M.
PETERSEN K D.
WISSENBACH M.
                                                                                                                                                                                    *tag=
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(WISS/)
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(WEST/)
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Wissenbach M;

Petersen KD,

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
           oligonucleotides (16-mers compared to 20-25-mers), therefore having increased specificity and affinity for survivin mRNA, and also have higher biostability and cell permeability. The present sequence represents an antisense oligonucleotide targeted to the human survivin CDNA target sequence shown in ADW09443 used in an example of the
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10022.
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of the invention are shorter than prior art survivin antisense
                                                                                                                                                   DB 1; Length 16; 92;
                                                                                                                                                                                 Indels
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                                                                                                                                                                                 ;
                                                                                                                      Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                   Query Match 15.6%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 92; Matches 12; Conservative 0; Mismatches
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2000GB-00024263.
2001WO-US000661.
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2001WO-US000668
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30-JAN-2001;
30-JAN-2001;
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04-OCT-2000;
30-JAN-2001;
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                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                        ABN10030;
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                                                                                                                                                                                                                                                                                           RESULT 101
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hgDMLP-1 mucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 provide initial substrates for the recombinant engineering of hGDMLP-1 corporations, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically of hGDMLP-1 proteins, as specifically concentration and/or amount specifically of hGDMLP-proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as character in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The collisorder associated with the expression of hGDMLP-1 may be used for diagnosing a disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO capture in the present sequence in the present sequence.
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hGDMLP-1 agoniat hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
skeletal muscle function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12; DB 1; Length 17;
Pred. No. 98;
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100.0%; Pred. No. 20.
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2000US-0236359P
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Best Local Similarity
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JI Y.
PENN S G.
HANZEL D K.
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27-SEP-2000;
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(PENN/)
(HANZ/)
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The invention relates to a novel polypeptide (I) comprising a sequence (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully defined in the specification, a fragment of at least 8 amino acids of (S1), 95% deviation from (S1) which are conservative substitutions, and es% identity to (S1). A polypetide of the invention acts as a agonist or antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity of hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.
                                                                                                                             Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                  Shannon MB;
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                                                                                                                                                                                                                                                                                                                                                                                                          invention for scanning the sequence represented in ACN63103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 17; 98;
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                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                  Rank D,
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                                                                                                                                                                                                            Disclosure; SEQ ID NO 10022; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.6%; Score 12; 100.0%; Pred. No.
                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 22; 94pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.6
Best Local Similarity 100.
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 TCTGGAGTCCTC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 rcredadrecre 17
                                                                 Ji Y, Penn SG,
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                                    SHANNON M E.
                                                                                                 WPI; 2004-533378/51.
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RANK D.
CHEN W.
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                                                                                                                                                                                 Eunction |
   (RANK/)
(CHEN/)
                                    (SHAN/)
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                                                             Gu Y,
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a neovascular condition of the retina,

hyperneovascular condition such as

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The present invention relates to the human uncoupling protein 3 (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The polymorphisms are associated with obesity, especially diabetes mellitus associated obesity. They polymorphisms may be identified and analysed to determine whether an individual is susceptible to obesity and may be used as the basis for targeted design of drugs to treat obesity. The present sequence was used in the identification and amplification of UCP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplama; kidney disease; neobacular condition; hyperplama; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                    ö
                                                                                                                                                                                Score 11.8; DB 1; Length 15;
Pred. No. 92;
0; Mismatches 2; Indels
                                                                                                                                                   Sequence 15 BP; 4 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 80; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MURD-) MURDOCH CHILDRENS RES INST
                                                                                                                                                                                                                                                                                                                                                                 AAF52028 standard; DNA; 15 BP
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                                                                                                                                                                                15.3%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                  44 GGTAAAGAGCCAGCG 58
                                                                                                                                                                                                                                                                                 GGCACAGAGCCAGCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligonucleotide #2988
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                    13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-041421/05.
                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                     polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                 AAF52028;
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                    Matches
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inhibiting or reducing growth factor mediated cell proliferation, oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F5151). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a 3' fragment of the dUTPase (DU) gene coding sequence of equine infectious anemia virus (EIAV). In the mutated EIAVGeleudu gene of the invention, this portion of the DU gene is ligated to a 5' fragment (see ABL53809) of the gene, to produce a DU gene-deleted construct (see ABL53811). The invention describes a vaccine for effectively and safely immunising mammals, especially equids, from disease caused by BIAV, the vaccine being tested for efficacy or immunogenicity using an EIA equine challenge model of the invention. The vaccine is a gene-deleted BIAV, each of gene-deleted EIAV, which lacks the ability to express the mutated gene protein in vivo, this lack of expression being useful to differentiate vaccinated from non-vaccinated or infected mammals. The multiple low dose EIA challenge model of the invention can be used to determine the efficacy of vaccines, treatments and diagnostic tests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           does not include a start or stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reproduce natural infection model which is useful for evaluating immunogenicity of BIAV vaccine, involves administering a median horse infective dose to equine.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIAV; dUTPase; enzyme; DU gene; vaccine; infection; model; gene; ss.
              brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown KK;
                                                                                                                                                                                                                                                                                                                                                                                                                     Equine infectious anemia virus DU gene coding sequence 3' fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infecting equine with equine infectious anemia virus in order to reproduce natural infection model which is useful for evaluating
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                                                                                                                ch 15.3%; Score 11.8; DB 1; Length 15; 1 Similarity 86.7%; Pred. No. 92; 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issel C, Hennessey KJ,
                                                                                 Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "S2 peptide"
/note= "the CDS does no
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                                                  vessels or any other hyperplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equine infectious anemia virus
                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                          68
                                                                                                                                                                                                                          CAGCGCTGCTGATGT 15
                                                                                                                                                                                                                                                                                                               ABL53810 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                          54 CAGCGAAGCTGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-339776/37.
P-PSDB; ABB75741.
                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                  ABL53810;
                                                                                                                                                                                                                                                                               RESULT 105
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ABL53795 standard; DNA; 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, single nucleotide polymorphism; SNP; RANGAP1;
haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1;
genotyping; cancer; irregular cell cycle associated disorder; ASO; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genotyping human Ran GTPase activating protein 1 gene of individual for determining haplotype of individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SNPB) in the human Ran GTBase activating protein 1 (RANGAPI) gene located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or genotyping the RANGAPI gene. The methods of the invention make use of allele-specific oligonucleotides (ASOB) as probes and primers and/or primer-extension oligonucleotides for detecting the RANGAPI gene polymorphisms. The polynucleotides and screened compounds are useful for treatment of diseases associated with RANGAPI activity, such as cancer and other disorders associated with an irregular cell cycle. AAS19704-AAS19742 represent ASO probes for detecting human RANGAPI gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to novel single nucleotide polymorphisms
                                                                                                                                       Gaps
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                                                                     DB 1; Length 15;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASO probe #28 to detect human RANGAP1 gene polymorphisms.
                                                                                                                                    2
Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
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                                                              Score 11.8; Di
Pred. No. 92;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; allele-specific oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 14; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS19731 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2000; 2000US-0198072P.
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                                                              Query Match 15.3%;
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                 AGACAGCCTTGGGAT 15
                                                                                                                                                                                                   7 AGACGGCCTGGGGAT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS19731;
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                                                                                                                                                                                                                                                                                                                                                            RESULT 106
AAS19731
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Novel vaccine comprising gene-mutated equine interlibe measure which lacks ability to express mutated gene protein in vivo, useful for immunizing horses against disease caused by equine infectious anemia

3xample 6; Fig 5; 54pp; English.

F, Issel C, Hennessey KJ, Brown KK;

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'n

Puffer

Montalaro RC,

WPI; 2002-339773/37. P-PSDB; ABB75736.

/note= "the CDS does not include a start or stop codon"

06-SEP-2001; 2001WO-US027601.

09-SEP-2000; 2000US-00658547.

(ALKU ) AKZO NOBEL NV

/\*tag= a /product= "82 peptide" Location/Qualifiers

/partial

40200220041-A2

14-MAR-2002

enzyme; DU gene; vaccine; diagnosis; gene; ss.

Squine infectious anemia virus.

Cos

dUTPase;

Squine infectious anemia virus DU gene 3' fragment

(first entry)

25-JUN-2002

ABL53795

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The present sequence is a 3' fragment of the dUTPase (DU) gene coding sequence of equine infectious anemia virus (SIAV). In the mutated ELAVACELLEDU gene of the invention, this portion of the DU gene is ligated to a 5' fragment (see ABLS3794) of the gene, to generate the sequence of given in ABLS3796. Two Styl sites flanking the gene are used to create the deletion, removing 80% of the DU coding sequence, including 4 of 5 conserved amino acid motifs. The invention relates to ElA vaccines that provide immunity to mammals, especially to equines, from infection with provide immunity to mammals, especially to equines, from infection with the ELAV, and which allow differentiation between vaccinated and nonvaccinated, but exposed, animals. The vaccine has at least 1 mutation in the ELAV, e.g. the present DU gene-mutated ELAV construct, which produces not reduce the ability of the mutated ELAV construct, which produces not reduce the ability of the mutated ELAV replicate in cell culture, allowing large-scale vaccine production. The vaccine cannot cause constraind disease or spread to other animals. The mutated region can also be used as an insertion point for foreign genes, using ELAV as a vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AGACGGCCTGGGGAT 21
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ACF57576 standard; DNA; 15 BP

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Gaps

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Score 11.8; DB 1; Length 15; Pred. No. 92; 0; Mismatches 2; Indels

86.78;

Best Local Similarity Matches 13; Conserv

Query Match

72

58 GAAGCTGATGTCCTG 13; Conservative

8

GAACCTGSTGTCCTG 15

RESULT 107 ABL53795

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Dean C, Heidaran M, Spargo CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of human fructose-bisphosphate aldolase B (ALDOB) and single nucleotide bolymorphisms (SNRs) which have been identified in each sequence. The method of haplotyping the sequences is useful for haplotyping the fructose-biphosphate aldose B (ALDOB) gene of an individual or for validating the ALDOB protein as a candidate target for treating a medical condition predicted to be associated with ALDOB activity. The present sequence is an allele-specific primer/probe used to identify the haplotype of the human ALDOB gene in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                  Human ALDOB gene allele-specific primer SEQ ID NO: 27
                                                                                                                                        Human; ALDOB; fructose-bisphosphate aldolase B; SNP; single nucleotide polymorphism; primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 39; Page 14; Opp; English
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                                                                                                                                                                                                                                                                                                                                                                                                        (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                        26-APR-2002; 2002WO-US013328.
                                                                                                                                                                                                                                                                                                                                                                  26-APR-2002; 2002WO-US013328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ82347 standard; DNA; 15
                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-877338/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kazemi A,
                                                                                                                                                                                                                                           WO2003091454-A1
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                                                                                                                                                                                                     Homo sapiens
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                                                            22-APR-2004
                                                                                                                                                                                                                                                                                   06-NOV-2003.
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                    ACP57576
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                                                                                                                                                               New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 4 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
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Pred. No. 92;
0; Mismatches
                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 128; 48pp; English.
                                                                                            Spargo CA;
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                                   (BECT ) BECTON DICKINSON & CO. (HAAL/) HAALAND P D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%;
28-NOV-2001; 2001US-0333476P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGCTTATCTCCTAT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 86.7
es 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AAGCTGATGTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding the P3 peptide
                                                                                          Dean C, Heidaran M,
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                                                                                                                                WPI; 2003-505179/47.
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useful for inhibiting tumor fibrotic disorders, proliferative (angiogenic)

Seguence 15 BP; 5 A; 2 C; 3 G; 5 T; 0 U; 0 Other; New peptides having growth inhibitory action, or cancer cell proliferation, or for treating myeloproliferative diseases, and blood vessel disorders. Disclosure; SEQ ID NO 178; 48pp; English WPI; 2003-505179/47. Local Similarity WO2003045973-A2 angiogenesis 13; 06-MAY-2004 05-JUN-2003 Synthetic. 29 ADJ82379; Query Match RESULT 111 Matches ADJ82379 à 셤 

15.3%; Score 11.8; E 86.7%; Pred. No. 92; tive 0; Mismatches AAGCTGATGTCATAT 15 AAGCTGATGTCCTGT Conservative

KLMSY-encoding nucleotide #107. ADJ82379 Btandard; DNA; 15 (first entry)

BP

ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; cardinoma; sarcoma; osteosarcoma; glioma; melanoma; mycoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;

30-SEP-2002; 2002WO-US031165.

28-NOV-2001; 2001US-0333476P.

(BECT ) BECTON DICKINSON & CO (HAAL/) HAALAND P D.

Heidaran M, Dean C,

Spargo CA;

WPI; 2003-505179/47.

New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (anglogenic)

The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGP-R) is activated in an autocrime manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Lys-Lys-Bhe-Phe-His-Pro-Val (FS). [I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, carcoma, osteosarcoma, glicoma, melanoma, myroma, adenoma, neuroblastcoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders myeloproliferative diseases, and blood vessel proliferative (anglogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide. Gaps ö 15.3%; Score 11.8; DB 1; Length 15; 86.7%; Pred. No. 92; 2; Pred. 0; Mismatches 2; Indele Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other; Disclosure; SEQ ID NO 160; 48pp; English 13; Conservative Best Local Similarity disorders. Query Match Matches 

59 AAGCTGATGTCCTGT 73 1 AAGCTAATGTCCTAT 15 셤 ò

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ADJ82331 standard; DNA; 15 BP KLMSY-encoding nucleotide #59. 06-MAY-2004 (first entry) ADJ82331; 

RESULT 112 ADJ8233

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Gaps

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DB 1; Length 15; 2; Indels ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteocaarcoma; melanoma; mycoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis.

Synthetic

WO2003045973-A2.

05-JUN-2003

28-NOV-2001; 2001US-0333476P

30-SEP-2002; 2002WO-US031165

(BECT ) BECTON DICKINSON & CO. (HAALAND P D.

Spargo CA Dean C, Heidaran M,

WPI; 2003-505179/47.

useful for inhibiting tumor fibrotic disorders, proliferative (angiogenic) New peptides having growth inhibitory action, or cancer cell proliferation, or for treating myeloproliferative diseases, and blood vessel

Disclosure; SEQ ID NO 112; 48pp; English

The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in

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an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Lys (P2) App-Asp-Clu-Clu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Via) (P3) (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative encoding the P3 peptide.
  a platelet-derived growth factor receptor (PDGF-R) is activated in
     which
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Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

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Gaps
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 DB 1; Length 15;
                         2; Indels
15.3%; Score 11.8; D
86.7%; Pred. No. 92;
tive 0; Mismatches
                                                  59 AAGCTGATGTCCTGT 73
                                                                       AAACTGATGTCCTAT 15
                          Conservative
            Local Similarity
les 13; Conserv
  Query Match
               Best Loca
Matches
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ADJ82363 standard; DNA; 15 ADJ82363; RESULT 113 ADJ82363 

BP

KLMSY-encoding nucleotide #91. (first entry) 06-MAY-2004

ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carctinoma; myxoma; denoma; metanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; anglogenesis

Synthetic.

WO2003045973-A2

05-JUN-2003

30-SEP-2002; 2002WO-US031165.

28-NOV-2001; 2001US-0333476P.

(BECT ) BECTON DICKINSON & CO

(HAAL/) HAALAND P D.

Spargo CA; Heidaran M, Dean C,

WPI; 2003-505179/47

New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)

Disclosure; SEQ ID NO 144; 48pp; English.

disorders

The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys (P2) App-App-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,

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sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.
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G; 5 T; 0 U; 0 Other; Sequence 15 BP; 4 A; 4 C; 2

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Gaps
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Score 11.8; DB 1; Length 15;
Pred. No. 92;
0; Mismatches 2; Indels
 ch 15.3%;
1 Similarity 86.7%;
13; Conservative
                                                   73
                                                   59 AAGCTGATGTCCTGT
 Query Match
Best Local Similarity
Matches 13; Conserv
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1 AAGCTCATGTCCTAT 15

ADJ82387 standard; DNA; 15 BP. RESULT 114 

06-MAY-2004 (first entry) ADJ82387;

KLMSY-encoding nucleotide #115.

ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;

carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis.

Synthetic.

WO2003045973-A2

05-JUN-2003

30-SEP-2002; 2002WO-US031165

28-NOV-2001; 2001US-0333476P

BECTON DICKINSON & CO. BECT )

HAALAND P D.

(HAAL/)

Dean C, Heidaran M,

Spargo CA

WPI; 2003-505179/47.

New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)

Disclosure; SEQ ID NO 168; 48pp; English

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                                                                                                               DB 1; Length 15;
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                                                         Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
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                                                                                                               Score 11.8; DE Pred. No. 92; 0; Mismatches
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                                                                                                         15.3%;
86.7%;
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                                                                                                                                                                     13; Conservative
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encoding the P3 peptide.
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                                                                                                               Query Match
Best Local Similarity
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ADJ82399
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DB 1; Length 15;

Score 11.8; | Pred. No. 92;

15.3%; 86.7%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
                                                                                                                                                                                                                                                                             ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
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Gaps
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Pred. No. 92;
0; Mismatches 2; Indels
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 174; 48pp; English.
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                                                                                                                                                                                                                                             KLMSY-encoding nucleotide #121.
                                                                                                                                              BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BECT ) BECTON DICKINSON & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-2002; 2002WO-US031165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-2001; 2001US-0333476P.
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                                                                                                                                            ADJ82393 standard; DNA; 15
                                                                                                                                                                                                            06-MAY-2004 (first entry)
Conservative
                              59 AAGCTGATGTCCTGT
                                                            1 AAGCTGATGTCGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AAGCTGATGTCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding the P3 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heidaran M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-505179/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAALAND P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          WO2003045973-A2.
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                           ADJ82393;
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Matches
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mammals vaccinated with the gene-mutated constituted and a meableable level of the expression product or amount of the normal gene sequence in infected mammals) and a method of differentiating a vaccinated mammal comprishing obtaining a sample from a test mammal, and analysing the sample for the presence of a gene expression product normally produced by wild-type EIAV but not produced by the EIAV construct cited above). The two redundant stop codons are inserted into the S2 open reading frame at positions corresponding to amino acids Gly5 and Gly18. The stop codon does not affect normal expression of the convergence of a least 7 base pairs downstream of the stop codon of the second coding region of TAT. The deletion does not interrupt the splice donor 2 site downstream of the stop codon of the second coding region of The initiation codon of the Scopen reading frame. The generation of the initiation codon of the Scopen reading frame. The generation of the initiation codon of the Scopen reading frame. The generation of the initiation codon of the Popen reading frame. The generation of the initiation codon of the Scopen reading frame. The generation of the initiation coden of the State of the face of the face of the second coding region of a restriction endonuclease site where the restriction endonuclease is a molecular marker for differentiating between wild type EIAV and the construct is useful for immunising mammals (e.g. horses) against lentiviral diseases, particularly BIAV infection. The contemplated in the DU (dUTPase) game of EIAV. The present sequence is the wild-type EIAV DU 5' or 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a construct comprising a gene-mutated equine infectious anemia virus (BIAV) comprising two redundant stop codons and a deletion (in the S2 protein) where the virus lacks the ability to express the mutated gene protein in vivo and where the lack of expression can be used to differentiate vaccinated from non-vaccinated or infected mammals. Also included are a diagnostic test for differentiating mammals waccinated with the above construct from non-vaccinated mammals infected mammals (comprising one or more reagents for demonstrating the absence of a normal BIAV gene expression product or a normal gene sequence in mammals vaccinated with the gene-mutated construct and a measurable level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New construct comprising gene-mutated equine infectious anemia virus (EIAV) for providing immunity from diseases caused by EIAV and allowing diagnostic differentiation between vaccinated and non-vaccinated mammals
                                                                                                                                                                                                                                    EIAV; S2 protein; vaccine; envelope protein; Tat protein;
lentiviral disease; EIAV infection; ds; dUTPase; DU.
                                                                                                                                                                                       BIAV dUTPage (DU) C-terminal DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Fig 5; 31pp; English.
                                                                                                                                                                                                                                                                                                            Equine infectious anemia virus.
                                            ADT41519 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2000; 2000US-00658547.
26-JUN-2002; 2002US-00180626.
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                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Montelaro RC, Craigo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MONT/) MONTELARO R C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-774916/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRAIGO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADT41520
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                                                                                                                                           27-JAN-2005
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                                                                                           ADT41519;
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RESULT 117
                        ADT41519
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the sequence represents a consensus 16 base pair repeat found in the human cytamegalovirus promoter regulatory region of the major immediate arrly gene, representing the nucleotides most frequently found within the 16n repeat. The promoter region contains the typical TATA and CAAT boxes and three different sets of repeat sequences, designated 19n, 18n and 16n repeats. Bach repeat sequence is repeated at least 4 times. There is a 2n repeat sequence splay a critical role in the relative level of expression of the downstream gene. Experiments using various deletions of the regulatory sequences suggest a direct correlation between the number of repeats and the relative level of gene expression. Hence these sequences or adjacent sequences constitute a component of the regulatory region that enhances the level of expression of the adjacent gene. These
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                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmids and DNA for transforming host cells - contain human cytomegalovirus immediate-early, promoter-regulatory DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                Human; cytomegalovirus; CMV; immediate-early; transcription; ss.
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                                         DB 1; Length 15;
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                                                                                                                                                                                                                                                                                                                  Consensus 16n repeat of major IR gene promoter region.
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7
            Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
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86.7%; Pred. No. 98;
cive 0; Mismatches
                                 ch 15.3%; Score 11.8; 1 Similarity 86.7%; Pred. No. 92; 13; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IOWA ) UNIV IOWA STATE RES FOUND INC.
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87US-00058662.
88US-00256134.
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                                                                                                     21
                                                                                                                                1 AGACAGCCTTGGGAT 15
                                                                                                                                                                                                         AAQ32194 standard; DNA; 16
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nes 13; Conservative
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                                                                                                     7 AGACGGCCTGGGGAT
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                                                       Local Similarity
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27-APR-1993
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                                                                                                                                                                                                                                          AAQ32194;
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                                          Query Match
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Matches
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                                                                     Matches
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30-JAN-1985;
22-MAY-1987;
05-OCT-1988;
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                                                                                                                                       US5385839-A.
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29-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                       Stinsk1 MF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ81490;
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                                                                    gene
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a 16 base pair repeat found in the human cytamegalovirus promoter regulatory region of the major immediate early gene from nucleotides -371 to -356 (distance from the cap site). The promoter region contains the trylical TMTA and CAAT boxes and three different sets of repeat sequences, designated 19n, 18n and 16n repeats Bach repeat sequence is repeated the repeat dequence and/or the sequence which is repeated twice. The repeat sequence and/or the surrounding sequences play a critical role in the relative level of expression of the downstream gene. Experiments using various deletions of the regulatory sequence suggest a direct correlation between the number of repeats and the relative level of gene expression. Hence these sequences constitute a component of the regulatory region that enhances the level of expression of the adjacent gene. These components are referred to as enhancers or adjacent sequences. See also AAQ32183-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmids and DNA for transforming host cells - contain human cytomegalovirus immediate-early, promoter-regulatory DNA sequence.
                                                                                                                                                                                                                          Human; cytomegalovirus; CMV; immediate-early; transcription; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 and AAQ32430-4. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                       l6n repeat of major IB gene promoter region.
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87US-00058662.
88US-00256134.
                                                              AAQ32195 standard; DNA; 16 BP.
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                                                                                                                                   (revised)
(first entry)
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22-MAY-1987;
                                                                                                                                   25-MAR-2003
27-APR-1993
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                                                                                                                                                                                                                                                             Synthetic.
                                                                                                  AAQ32195;
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                             RESULT 119
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                                                AAQ32195,
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AAQ81491 standard; DNA; 16

(revised)
(first entry)

25-MAR-2003 29-AUG-1995

AAQ81491;

RESULT 120
AAQ81491/c
1D AAQ81
XX
AC AAQ8:
XX
DT 25-M
DT 29-AI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New transfer vectors for gene expression – comprising the immediate-early promoter regulatory region of human cytomegalovirus.
                                     CMV; HCMV; major immediate-early; IB gene; IBPR; vector; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMV; HCMV; major immediate-early; IB gene; IBPR; vector; transcription;
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15.3%; Score 11.8; D
Best Local Similarity 86.7%; Pred. No. 98;
Matches 13; Conservative 0; Mismatches
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IEPR 16n repeat (-371 to -356).
                                                                                                                                                                                                                                                        85US-00696617.
87US-00058662.
88US-00256134.
90US-00582130.
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ID AAQ81490 standard; DNA; 16 BP.
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                                                             expression; pIEPR12; ss.
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87US-00058662
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(first entry)
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                                                                                                Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-081566/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1992;
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22-MAY-1987;
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88US-00256134. 90US-00582130.

05-OCT-1988;

10-SEP-1990;

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AAQ81478, enhances the transcription and expression of adjacent genes in human cells, and has been used to construct gene transfer vector pIEPR12 (NRKL B-15930). The IEPR region includes 19n, 18n and 16n repeat sets, each repeated 4 times, and a 21n set repeated twice. The 16n set is given in AAQ81491-94, with the consensus in AAQ81490. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New retroviral vectors, particularly for gene therapy - which are free of
the gag coding sequence, to provide for high levels of gene expression,
viral titre and packaging efficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The fusion sites AAV26756-V26760 were used in the production of two retroviral vectors (RV). The first is a RV that has no gag coding sequence is capable of delivering a gene of interest to a target cell when packaging functions of gag, pol and env are provided. The second is a RV based on murine leukaemia virus (MLV) where entire gag and env coding sequences are completely deleted. The vectors can be used for gene
                                                                                                                                    New transfer vectors for gene expression - comprising the immediate-early promoter regulatory region of human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                вв; gag; gene delivery; pol; env; murine leukaemia virus; gene therapy
                                                                                                                                                                                                               HCMV immediate-early promoter regulatory (IEPR) region, shown in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytomegalovirus immediate-early promoter fusion site 16.
                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 11.8; Pred. No. 98;
                                           (IOWA ) UNIV IOWA STATE RES FOUND INC.
                                                                                                                                                                                  Disclosure; Fig 3; 10pp; English.
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robbins PD;
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                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
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                                                                                                       WPI; 1995-081566/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9812338-A1
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                                                                           Stinski MF;
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Gaps

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The invention relates to single nucleotide polymorphisms in the gene encoding human 5-hydroxytryptemine (serotonin) receptor 5A (HTRSA). A method for haplotyping the HTRSA gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the HTRSA haplotypes given in the specification or whether both copies the HTRSA haplotype pairs can be assigned to specific genotypes. An association between a trait and a haplotype or haplotype pairs can be identified by comparing the frequency of the haplotype pair in a population exhibiting the trait with the haplotype or haplotype pair in a population exhibiting the trait with the haplotype or haplotype pair in a population of the haplotype or haplotype pair in a population of the haplotype or haplotype pair in a population in a reference the trait is associated with the haplotype or haplotype pair. HTRSA and its corresponding DNA are used for studying the expression and in screening for candidate drugs to treat diseases related to HTRSA activity, such as neurological disorders, including depression and epilepsy. Sequences ABK72139-ABK72358 represent allele-
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therapy, for example for the delivery of hormones, enzymes, receptors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel genetic variants of 5-Hydroxytryptamine (Serotonin) Receptor 5A isogenes, useful for improving efficiency and reliability in drug development for treating neurological diseases.
                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; neurological disease; depression; epilepsy; gene therapy; single nucleotide polymorphism; haplotype pair; chromosome 7q36.1.
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                                                                                         Score 11.8; DB 1; Length 16;
Pred. No. 98;
                                                                                                                             Indels
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                                                     Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other
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                                                                                                                             0; Mismatches
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                                                                                       ch 15.3%;
1 Similarity 86.7%;
13; Conservative
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                                                                                           Query Match
Best Local Similarity
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Wed Apr 19 16:15:55 2006

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2. Homo sapiens

18-OCT-2001

Oligonucleotide SEQ ID NO 41787 for detecting SNP TSC0012525

21-FBB-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                   Oligonucleotide SEQ ID NO 184442 for detecting SNP TSC0045516,
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Best Local Similarity 92.3%; Pred. No. 90;
Matches 12; Conservative 0; Mismatches 1; Indels
       Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 184442; 29pp + Sequence Listing; German.
                                       0; Indels
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     DB 1;
   Score 11.6; DB
Pred. No. 98;
1; Mismatches
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                                                                                                                                                                                                                                                                 (first entry)
                                     11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
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Query Match
Best Local Similarity
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0; Mismatches
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nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation status.
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Gaps

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ABC41770 standard; DNA; 13 BP.

RESULT 125 ABC41770 ID ABC4177

39 TGAGAGGTAAAGA 51

TGAGATGTAAAGA 1

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                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 184441; 29pp + Sequence Listing; German.
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1 Similarity 92.3%;
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Best Local Similarity
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1D ABC4177

AC ABC
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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useful in expression vectors for high yield prodn. of activator by large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The probe is used in an example to exemplify the cloning of TPA gene. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of probe for human tissue plasminogen activator (TPA) gene.
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igonucleotides, useful for diagnosis and cell typing, it detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 11.4; DB 1; Length 13; 92.3%; Pred. No. 90; ive 0; Mismatches 1; Indels
                                                                                                                      Claim 1; SEQ ID NO 41788; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 BP; 2 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KANEGAFUCHI KAGAKU KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombolytic; enzyme; protease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN70550 standard; DNA; 14 BP.
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86JP-00020469.
86JP-00097481.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scale suspension culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 TGAGAGGTAAAGA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 92.3
hes 12; Conservative
      Set of oligonucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 TGAGAGGTAAGGA 1
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                                                            methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-1985;
31-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-1986;
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29-APR-1991
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Gaps

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Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityrissis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatoosis, neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplama; kidney disease; neovascular condition; hyperplama; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-IR Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBD], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF4515.1 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ruba, pilaris, serbornhoea, kelolids, keratosis, neoplasis, scleroderma, warts, benign growths, cancers of the skin, a hyperneovasqular condition such as a neovascular condition of the retina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brain or skin, growth factor-mediated malignancies, other scierotic disease, kidney disease, hyperproliferation of the inside of blood
                                    Score 11.4; DB 1; Length 14;
Pred. No. 98;
0; Mismatches 1; Indels
Sequence 14 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edmondson SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sxample 7; Page 58; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vessels or any other hyperplasia
                                                                                                                                                                                                                                                     AAF48760 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                         IGFBP3 oligonucleotide #2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0140345P.
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                                      14.8%;
92.3%;
                Query Match
Best Local Similarity 92.33,
Best Local 12; Conservative
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                 60 AGCTGATGTCCTG 72
                                                                                                                                                      2 AGCTGATGCCCTG 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
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                                                                                                                                                                                                                                                                                            AAF48760;
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                                                                                                                                                                                                                                                                                         Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant; virucide, ophthalmological, keloid, skin disorder, Insulin-like Growth Factor. I receptor; IGF-1; pityriasis; IGF binding protein, IGFB-2; IGFBP3; inflammation, psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; schorrhoes; ruba; keratosis, neoplasis; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperpleasis, kidney disease; necovascular condition; hyperpleasis, kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Werther GA, Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 58; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vessels or any other hyperplasia
                                                                                                                                      BP
                                                                                                                                                                                                                                                          IGFBP3 oligonucleotide #2178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-2000; 2000WO-AU000693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0140345P
                                                                                                                                      AAF48758 standard; DNA; 15
                                                                                                                                                                                                                   30-MAR-2001 (first entry)
31
                                     GATACAACTGTGG 13
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19 GATACAACTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-041421/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200078341-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation.
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Matches
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Score 11.4; DB 1; Length 15; Pred. No. 1.1e+02;

14.8%; 92.3%;

Best Local Similarity

Query Match

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GATACAACTGTGG 15
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RESULT

AAF48759 standard; DNA; 15 BP

AAF48759;

(first entry) 30-MAR-2001 GFBP3 oligonucleotide #2179.

Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityrlasis; IGF binding proctein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keardosis, neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neobascular condition of the retina; ss.

Homo sapiens

WO200078341-A1.

28-DEC-2000.

21-JUN-2000; 2000WO-AU000693

21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Wraight CJ, Werther GA,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 58; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an entitle ene oligonucleotide, (for Insulin-like Growth Factor [IGP]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which essent invention (see AAF45151 and AAF45153-F4516). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a neoplasias, sinch factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia AAP48759

AAP487

Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

GATACAACTCTGG 31 13

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Local Similarity 92.3

Matches

Query Match

GATACAACTGTGG 14 N

ADV37029 standard; RNA; 15 BP. 

(first entry) 10-FEB-2005 Human anti-HER2 NCH ribozyme substrate sequence #908.

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLM; presentilin-1; ps-1; presentilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; harpin; NCH; incyme; G-cleaver; amberzyme; Zinzyme; DNAzyme; cancer; heart cancer; Alzhaimer's disease; disbetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

Homo sapiens.

WO200116312-A2

08-MAR-2001

30-AUG-2000; 2000WO-US023998

31-AUG-1999 27-SEP-1999 27-SEP-1999

99US-0166543. 99US-0156236P. 99US-0156436P. 99US-0169100P. 99US-014432. 99US-0173612P. 99US-0173612P. 200US-00531025. 27-SEP-1999

06-DEC-1999; 29-DEC-1999; 29-DEC-1999; 08-NOV-1999

04-FEB-2000; 30-DEC-1999;

2000US-0197769P. 09-AUG-2000; 2000US-00636385 20-MAR-2000; 14-APR-2000; 23-MAY-2000;

(RIBO-) RIBOZYME PHARM INC.

Chowrira B; Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Ch Beaudry A, Zinnen S, Lugwig J, Sproat BS; Stinchcomb D, Mcswiggen J, Karpeisky A,

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 7; Page 490; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBT), protein Kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (pg-2), and hepaticis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-dreaver, amberzyme, cinclude hammerhead (HH), hairpin, NCH (inozyme), G-dreaver, amberzyme, cinclude hammerhead diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatitis and hepatitis and hammerhead as carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased

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Gaps ö

14.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels

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ABN80560 standard; DNA; 15
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                                                                                ABN80560;
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     ABN80560/C

MAC ABN80

MAC ABN80

MAC ABN80

MAC BBN

MAC
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cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for an anti-HER2 NCH ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein, gene and cDNA sequences of human colony stimulating factor 3(granulocyte) CSF3. Also described are single nucleotide polymorphisms (SNPs) identified within these sequences. The sequences can be used in the treatment of neutropenia, promyelocytic leukaemia and haematological disorders. The present sequence is an allele specific primer used to isolate the coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New variants of colony stimulating factor 3 (CSF3) isogenes, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; colony stimulating factor 3(granulocyte); CSP3; SNP; isogene; chromosome 17q11-12; single nucleotide polymorphism; immunostimulant; neutropenia; promyelocytic leukaemia; haematological disorder; gene therapy; PCR; prime; ss.
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         improving efficiency and reliability in the development of drugs for treating diseases associated with CSP3 activity e.g. neutropenia.
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                      14.8%; Score 11.4; DB 1; Length 15; 69.2%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 11.4; DB 1; Length 15; 80.0%; Pred. No. 1.1e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CSF3 gene allele specific primer SEQ ID NO: 18
                                                                                                                                                        Sequence 15 BP; 3 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 2 A; 1 C; 9 G; 2 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sausker EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 13; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL48040 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Messer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-2001; 2001WO-US018813
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Conservative
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                                                                                                                                                                                                                                                                                                                                  UGGAGCCCUCUGA 13
                                                                                                                                                                                                                                                                                                         29 TGGAGTCCTCTGA 41
                                                                                                                                                                                                                                                          9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL48040;
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AAL48040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genetic variants comprising haplotypes of the P450 (cytochrome) oxidoreductase (POR) isogene, useful in improving the efficiency of drug screening protocols for compounds targeting POR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                 Human, P450 (cytochrome) oxidoreductase, POR, cancer, haplotype, SNP, single nucleotide polymorphism; flavoprotein; enzyme, probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
Human P450(cytochrome) oxidoreductase allele specific probe #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Меввег С,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 14; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lanz EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLMSY-encoding nucleotide #76.
                                                                                                                                                                                                                                                                                                                                                                                               (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВЪ
                                                                                                                                                                                                                                                                                       01-OCT-2001; 2001WO-US030877.
                                                                                                                                                                                                                                                                                                                                           29-SEP-2000; 2000US-0236449P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AGCCAGCGAAGCTGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ82348 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kazemi A, Kliem SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-394236/42.
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AGAGGGCTGGGGRT 15 7 AGACGGCCTGGGGAT 21

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RESULT 134

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The invention relates to an isolated peptide or polypeptide (1) of no more than about 50 amino acid residues which when contacted with cells in which a platehet-derived growth factor receptor (PDGFR.) is activated in an autocrine manner, inhibits the growth of these cells. The isolated in an autocrine manner, inhibits the growth of these cells. The isolated competides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys (PA) App-App-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-His-Pro-Val (P5). (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, arcoma, osteosarcoma, glioma, melanoma, menoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, mysloproliferative diseases, and blood vessel proliferative (anglogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.
                                                                                                                                                                                                                                  New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 1.1e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 4 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 129; 48pp; English.
                                                                                                                                                              Spargo CA;
                                                                                                      (BECT ) BECTON DICKINSON & CO (HAALAND P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLMSY-encoding nucleotide #92
                                   30-SEP-2002; 2002WO-US031165.
                                                                       28-NOV-2001; 2001US-0333476P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-2002; 2002WO-US031165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGCTTATGTCCT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AAGCTGATGTCCT
                                                                                                                                                              Dean C, Heidaran M,
                                                                                                                                                                                            WPI; 2003-505179/47
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                                                                                                                                                                                                                                                                                        disorders.
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                                                                                                                            New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; canc carcinoma; asrcoma, myxoma; glioma; melanoma; myxoma; denoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease;
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                                                                                                                                                                                                                                                                                                     Score 11.4; DB 1; Length 15; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                   Sequence 15 BP; 4 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                              Disclosure; SEQ ID NO 145; 48pp; English.
                            Spargo CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spargo CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLMSY-encoding nucleotide #116.
(BECT ) BECTON DICKINSON & CO.
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                                                                                                                                                                                                                                                                                                     y Match 14.8%;
Local Similarity 92.3%;
hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                          59 AAGCTGATGTCCT 71
                                                                                                                                                                                                                                                                                                                                                              1 AAGCTCATGTCCT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BECT ) BECTON DICKINSON
                                                                                                                                                                                                                                                                 encoding the P3 peptide
                            Heidaran M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dean C, Heidaran M,
         HAALAND P D.
                                            WPI; 2003-505179/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAALAND P D
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         (HAAL/)
                            Dean C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HAAL/)
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WPI; 2003-505179/47

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The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGP-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Asp-Glu-Glu-Lys (P2) Lys-Lew-Het-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Fro-Val (P5) (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, carchoma, osteosarcoma, osteosarcoma, machanoma, machanoma, neuroblastema, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (anglogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.
                     New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic)
                                                                                                                                                                        Disclosure; SEQ ID NO 169; 48pp; English.
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                                 14.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                          59 AAGCTGATGTCCT 71
                                                                        12; Conservative
                                   Query Match
Best Local Similarity
                                                                       Matches
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KLMSY-encoding nucleotide #122.
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AAGCTGATATCCT 13
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ADJ 82394
1D ADJ 82394
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cytostatic, platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis

Synthetic

WO2003045973-A2

05-JUN-2003.

30-SEP-2002; 2002WO-US031165. 28-NOV-2001; 2001US-0333476P. (BECT ) BECTON DICKINSON & CO (HAAL/) HAALAND P D.

Spargo CA; Dean C, Heidaran M,

WPI; 2003-505179/47.

New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

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The invention relates to an isolated peptide or polypeptide (1) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGP-R) is activated in autocrine manner, inhibits the growth of these cells. The isolated in autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys (PA) hap-Abp-Glu-Lys (P2) Exer-Lyr (P2) Phe-Phe-Phe-Liys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, arcoma, osteosarcoma, glidma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, mycloproliferative diseases, and blood vessel proliferative classing the P3 peptide.
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Disclosure; SEQ ID NO 175; 48pp; English.
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14.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 1.18+02; tive 0; Mismatches 1; Indels
                                                         59 AAGCTGATGTCCT 71
                                                                         AAGCTGATGTCTT 13
                Local Similarity 92.
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ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; mycoma; adenoma; neuroblactoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; KLMSY-encoding nucleotide #108. BP ADJ82380 standard; DNA; 15 (first entry) angiogenesis. 06-MAY-2004 ADJ82380; ADJ82380

(BECT ) BECTON DICKINSON & CO 30-SEP-2002; 2002WO-US031165. 28-NOV-2001; 2001US-0333476P WO2003045973-A2 05-JUN-2003 Synthetic. 

ð Heidaran M, Dean C,

(HAAL/) HAALAND P D.

WPI; 2003-505179/47.

useful for inhibiting tumor fibrotic disorders, proliferative (anglogenic) New peptides having growth inhibitory action, or cancer cell proliferation, or for treating myeloproliferative diseases, and blood vessel

Disclosure; SEQ ID NO 161; 48pp; English

The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which wan contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated

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peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Lys-lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, or vory, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                    14.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 1.16+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                          Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCTGATGTCCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGCTAATGTCCT 13
                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                           encoding the P3 peptide.
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 140
                                                                                                                                                                                                                                                                                                                                                                                           Matches
    856666666666655588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
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KLMSY-encoding nucleotide #60. ВÞ ADJ82332 standard; DNA; 15 (first entry) 06-MAY-2004 ADJ82332; AD782332
AD782332
AD782332
AD782332
AD78232
AD

88; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; cardinoma; sarcoma; osteosarcoma; glioma; melanoma; mycoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis

Synthetic

WO2003045973-A2

05-JUN-2003.

30-SEP-2002; 2002WO-US031165.

28-NOV-2001; 2001US-0333476P.

(BECT ) BECTON DICKINSON & CO (HAALAND P D.

Dean C, Heidaran M,

Spargo CA;

WPI; 2003-505179/47.

New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

Disclosure; SEQ ID NO 113; 48pp; English.

The invention relates to an isolated peptide or polypeptide (I) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell prollferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

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ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.
                                                                                                                                                                       Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other
              ឧស្សន្តន្តន្
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Gaps ö 14.8%; Score 11.4; DB 1; Length 15; 92.3%; Pred. No. 1.1e+02; Indels 0; Mismatches Best Local Similarity 92.3 Matches 12; Conservative Query Match

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AAACTGATGTCCT 13 59 AAGCTGATGTCCT 71 셤 ð

ADJ82398 standard; DNA; 15 BP

ADJ82398;

(first entry) 06-MAY-2004 KLMSY-encoding nucleotide #126.

ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; cardinoma; sarcoma; osteosarcoma; glioma; melanoma; mycoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis. 

Synthetic

WO2003045973-A2.

05-JUN-2003

30-SEP-2002; 2002WO-US031165.

28-NOV-2001; 2001US-0333476P.

(BECT ) BECTON DICKINSON & CO (HAAL/) HAALAND P D. Spargo CA Dean C, Heidaran M,

WPI; 2003-505179/47.

New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

Disclosure; SEQ ID NO 179; 48pp; English.

The invention relates to an isolated peptide or polypeptide (1) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGFR) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys (P4) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Rhe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, orthograrcoma, osteosarcoma, glioma, melanoma, meyone, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

(first entry)

Sequence 15 BP; 5 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

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ADE13707 standard; DNA; 16 BP
                                                                           29-JAN-2004
                                                     ADE13707;
        RESULT 143
                    ADB13707,
                               The present sequence represents a polymucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex stability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test sequences to an aqueous medium containing double-stranded DNA test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the presence of the DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting the presence of the DNA test sequence) but also detection of
                               ö
                                                                                                                                                                                                                            Triplex formation; DNA detection; triple helix; identification; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify
                               Gaps
                               ô
                                                                                                                                                                                                    Triple helix third strand of c-myc gene nucleotides 2055-2070.
   Score 11.4; DB 1; Length 15;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 BP; 0 A; 9 C; 0 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 13-14; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          (PROF-) PROFILE DIAGNOSTIC SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oncogenes and Hepatitis B virus
                                                                                                                                  AAX14617 standard; DNA; 16 BP.
      14.8%;
                                                                                                                                                                                                                                                                                                                                            93US-00173489.
                                                                                                                                                                                                                                                                                                                                                                   92US-00968436.
                                                                                                                                                                                (first entry)
Query Match
Best Local Similarity 92.3'
                                                   59 AAGCTGATGTCCT 71
                                                               1 AAGCTGATGTCAT 13
                                                                                                                                                                                                                                       oncogene; virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 Wang C;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-130384/11.
                                                                                                                                                                                24-MAR-1999
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                            22-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                   29-0CT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                  Hepburn AG,
                                                                                                                                                                                                                                                                                              US5861244-A.
                                                                                                                                                                                                                                                                                                                     19-JAN-1999.
                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                         AAX14617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteria.
                                                                                                           RESULT 142
                                                                                                                       AAX14617
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The invention describes an oligonucleotide comprising 10-100 bases, in which at least 2 bases are juxtaposed universal bases. Also disclosed is a method for detecting a polymorphism in a genetic material comprising contacting a DNA with the new oligonucleotide, and identifying whether the oligonucleotide bound to the DNA. The novel oligonucleotide is used for diagnostic purposes, e.g. detection of single nucleotide polymorphisms (SNPS). It is also applicable in array technology, sequencing, and shoridisation. The method increases the ability to differentiate a single nucleotide polymorphism or a polymorphic site from a normal site and allows the development of more efficient diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                          polymorphism detection; diagnostic; ingle nucleotide polymorphism detection; SNP detection; array technology; sequencing; hybridisation; 88; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligonuclectide for diagnostic purposes, e.g. detection of single nuclectide polymorphisms, comprises universal and generic bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and therapeutics. This sequence represents an oligonucleotide of the invention. Note: This sequence differs from the sequence given in the examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Oligonucleotide probe for diagnostic purposes seq id 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 BP; 3 A; 4 C; 3 G; 4 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/mod_base= OTHER
/note= "OTHER= Not described"
                                                                                                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "OTHER= Not described"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 39; 37pp; English.
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1998; 98US-00136080.
18-JUL-2001; 2001US-0306229P.
08-MAY-2002; 2002US-00142729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2003; 2003US-00375504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0060673P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 GATACAACTCTGGAG 33
                                                                                                                                                                                                                                                                                                                   *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0°
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-830610/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown BD, Riley TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BROW/) BROWN B D. (RILE/) RILEY T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003170711-A1
                                                                                                                                                                                                                                                     Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                           modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-2003
                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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Gaps

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14.8%; Score 11.4; DB 1; Length 16; 92.3%; Pred. No. 1.1e+02; tive 0; Mismatches 1; Indel8

40 GAGAGGTAAAGAG 52

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14 GAGAGGGAAAGAG 2

Local Similarity 92.3 hes 12, Conservative

Matches

Query Match

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15 GATACNGCTCTNGAG 1

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The invention describes an oligonucleotide comprising 10-100 bases, in which at least 2 bases are juxtaposed universal bases. Also disclosed is a method for detecting a polymorphism in a genetic material comprising contacting a DNA with the new oligonucleotide, and identifying whether the oligonucleotide bound to the DNA. The novel oligonucleotide is used for diagnostic purposes, e.g. detection of single nucleotide is used polymorphisms (SNPs). It is also applicable in array technology, sequencing, and hybridisation. The method increases the ability to differentiate a single nucleotide polymorphism or a polymorphic site from a normal site and allows the development of more efficient diagnostics and therapeutics. This sequence represents an oligonucleotide of the invention. Note: This sequence differs from the sequence given in the
                                                                                                                                                                                                                                                                                                                                      polymorphism detection; diagnostic; ingle nucleotide polymorphism detection; SNP detection; array technology; sequencing; hybridisation; ss; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New oligonucleotide for diagnostic purposes, e.g. detection of single nucleotide polymorphisms, comprises universal and generic bases.
                                                                                                                                                                                                                                                                          Oligonucleotide probe for diagnostic purposes seq id 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 16 BP; 3 A; 4 C; 3 G; 4 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "OTHER= Not described"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "OTHER= Not described"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/mod_base= OTHER
                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-1997; 97US-0060673P.
18-AUG-1998; 98US-00136080.
18-JUL-2001; 2001US-0306229P.
08-MAY-2002; 2002US-00142729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2003; 2003US-00375504
                                                                      ADE13694 standard; DNA; 16
                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown BD, Riley TA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BROW/) BROWN B D. (RILE/) RILEY T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003170711-A1
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified_base
                                                                                                                                                                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                     ADE13694;
                            ME13694/
XX ADE1
XX Begu
XX XY BEGU
XX BEGU
XX
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel oligonucleotide probes and primers comprising universal and generic bases. The oligonucleotides of the invention are useful as primers and probes for diagnosing diseases, particularly in detecting polymorphism in a sample of genetic material and for diagnosing a genetic disease in a patient. The present sequence is a probe used to identify mutations or polymorphisms. This sequence used in the exemplification of the invention.
                                                                                                                                                                                                                                  numbers of 3-nitropyrrole group"
                                                                                                                                                                                                                                                           /*tag= b
/note= "Linked via 2 numbers of 3-nitropyrrole group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligonucleotides useful as primers and probes for diagnosing diseases, i.e. polymorphism in sample of genetic material, comprises bases where some are juxtaposed universal bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                    Diagnosis; polymorphism detection; genetic disease; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.8%; Score 11.4; DB 1; Length 16; 92.3%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
                                                                                                         Probe 6 #2 used to identify mutations or polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 4 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; SEQ ID NO 35; 18pp; English.
                                                                                                                                                                                                       4. .5
/*tag= a
/note="Linked via 3 m
12. .13
/*tag= b
                                                                                                                                                                                          Location/Qualifiers
                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  멾.
                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2001; 2001US-0306229P.
                                                                                                                                                                                                                                                                                                                                                         08-MAY-2002; 2002US-00142729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM83291 standard; DNA; 16
                           ADM83304 standard; DNA; 16
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 CTCTGAGAGGTAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCTGAGAGCTAA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown BD, Riley TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-787489/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
ses 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              (BROW/) BROWN B D. (RILE/) RILEY T A.
                                                                                                                                                                                                                                                                                                    US2003165888-A1
                                                                                                                                                               Unidentified
                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                              misc_feature
                                                                               03-JUN-2004
                                                                                                                                                                                                                                                                                                                               04-SEP-2003
                                                      ADM83304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM83291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 146
RESULT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM83291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SXXXE
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Local Similarity 80.0 les 12; Conservative

Query Match Best Local 8 Matches 12

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Gaps

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14.8%; Score 11.4; DB 1; Length 16; 80.0%; Pred. No. 1.18+02; tive 0; Mismatches 3; Indels

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The sequences given in AAT18103-11 are primers which may be used in the species-specific amplification of M. kansasii DNA. These primers bind to a fragment, bases 51-220, of the clone p6123. p6123 is a cloned probe which hybridises to all M. kansasii strains, including the subgroup which is negative to binding with the probe pWK1-9 (M.Yang et al. 1993. J. clin. Microbid. 31, 2769-2772). These primers are pref. used in strand displacement amplification (SDA). These primers showed a positive reaction with 74 M. kansasii isolates tested, but did not cross react with any other Mycobacterium species. In addition, these primers did not cross-react with Nocardia asteroides or Rhodococcus rhodochrous. This primer binds around bases 141-156 of the p6123 fragment
                                                                                                                                                                                                                                              Primers for species-specific amplification of Mycobacterium kansasii -detect double stranded target sequences with no cross-reactivity between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant replication-defective flavivirus; arthropod vector; 31 stem-loop structure substitution; Dengue virus type 2; DSN2; West Nile virus; WN; Flavivirus-induced infection; dengue fever; dengue haemorihagic fever; dengue shock syndrome; viructide; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%; Score.11.2; DB 1; Length 16; 81.2%; Pred. No. 1.2e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        West nile virus genome, nucleotides 1-16.
                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 17; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                94US-00308892
                                         94US-00308892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2001; 2001WO-US008686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2001; 2001WO-US008686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AACTCGACGCCTCGG 16
                                                                                                                     (BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS56009 standard; RNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AACAAGACGGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT OF HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                       WPI; 1996-171042/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     West Nile virus.
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                                                                                19-SEP-1994;
                                       19-SEP-1994;
  19-MAR-1996.
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07-JAN-2003
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                                                                                                                                                                  Spears PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS56009;
                                                                                                                                                                                                                                                                                            species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 148
8X#X#X#X#X#X####X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel oligonucleotide probes and primers comprising universal and generic bases. The oligonucleotides of the invention are useful as primers and probes for diagnosing diseases, particularly in detecting polymorphism in a sample of genetic material and for diagnosing a genetic disease in a patient. The present sequence is a probe used to identify mutations or polymorphisms. This sequence used in the exemplification of the invention.
                                                                                                                                                              i. .5
/*tag= a
/note= "Linked via 3 numbers of 3-nitropyrrole group"
                                                                                                                                                                                                                                        ^{\prime}+tag=" b" hinked via 2 numbers of 3-nitropyrrole group" note= "Linked via 2 numbers of 3-nitropyrrole group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligonucleotides useful as primers and probes for diagnosing diseases, i.e. polymorphism in sample of genetic material, comprises bases where some are juxtaposed universal bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species-specific amplification; M. kansasii; p5123; probe; pWKl-9; strand displacement amplification; SDA; primers; Mycobacterium; cross-react; Nocardia asteroides; Rhodococcus rhodochrous; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                        Diagnosis; polymorphism detection; genetic disease; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.8%; Score 11.4; DB 1; Length 16; 92.3%; Pred. No. 1.1e+02; tive 0; Mismatches 1; Indels
               Probe 6 #1 used to identify mutations or polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. kansasii species specific amplification primer. Dl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 BP; 4 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; SEQ ID NO 22; 18pp; English
                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2002; 2002US-00142729
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                                                                                                                                                                                                                      15. .16
/*tag= b
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-787489/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown BD, Riley TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BROW/) BROWN B D. (RILE/) RILEY T A.
                                                                                                                                                                                                                                                                                                           US2003165888-A1
                                                                                                                                                     misc_feature
                                                                                               Unidentified
                                                                                                                                                                                                                         misc_feature
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WPI; 2002-750556/81

JS5500341-A Synthetic

AAT18111;

RESULT 147

ሯ 셤 Zeng L;

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Gaps

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The present invention relates to a mutant replication-defective flavivirus having a genome with a 3' stem-loop structure substitution, and being defective for replication in an arthropod vector that transmits flavivirus to humans. The genome is selected from a first flavivirus and the 3' stem-loop structure from a second flavivirus, where the first flavivirus may be negrous is different from the second flavivirus, where the first flavivirus may be negrous is different from the second. For example the first flavivirus may be west nite for treating flavivirus-induced infections, particularly dengue fever or dengue haemorrhagic fever/shock syndrome. The present sequence represents a part of the My genome used to construct a mutant replication on 07-AUG-2003 to correct OS field.)
New mutant replicon-defective flavivirus having a genome with a 3' stem-
loop structure chimeric substitution useful as vaccine for treating
flavivirus-induced infection e.g. dengue fever, dengue hemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
HBV promoter; vancomycin-resistant enterococci promoter; VRB promoter;
wanh promoter; androgen receptor promoter; Apromoter;
human epidermal growth factor receptor 2 promoter; her? promoter;
beta lactamase promoter; Bla promoter; transgene; cancer; promoter; munucle cancer; immunological disorder; prostate cancer; cytostatic;
autoimmune diseas; HBV pre-S promoter; HBV-X promoter;
Bnterococcus infection; immunosuppressive; antibacterial; antiviral;
gene expression modulator; multiple sclerosis; MS;
chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
systematic lupus erythematosus; SLB; graft-vs-host disease; GVHD;
familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheppard LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 1.2e+02; tive 0; Mismatches 3; Indels
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MD, Latour DR, Thomas RL, Kongpachith A, She
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 BP; 7 A; 3 C; 4 G; 0 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Androgen receptor wild type HLH-3 sequence.
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                                                                                                                                     Example 3; Page 61; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 81.2%;
nes 13; Conservative
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                                                                                      fever/shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-130595/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 119
RESULT 119
ABKZ9916/C
XX
XX
ABKZ9916/C
XX
XX
CYC11N
XW
CYC11N
XW
HUMAN
XW
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Matches
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The invention describes an isolated nucleic acid regulatory sequence for a cyclin DI promoter, a CD40L promoter, vancomycin-resistant enterococci (VRB) promoter. Human epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase cyclin DI promoter. Transcription regulatory sequences may be used to require expression of the endogenous, autologous or heterologous genes operably linked to the promoter, and may be incorporated into heterologous nucleic acid constructs for use in regulated expression of transgenes. Regulated expression of cyclin DI can be used in cancer therapies, such as breast, colon or pancratic cancers and familial adenomatous polyposis. Regulation of the activity of CD40L gene promoter may be used in the treatment of immunological disorders, and as a utolimmune diseases e.g. multiple sclerosis (MS), systematic lupus crythematosus (SLB), graft-vs-host disease (GVHD) and rheumatold carthritis. Regulated expression of genes under the control of the HBV (hepatitis B)-specific core, pre-5 and X promoters can be used in the therapy of HBV disease, chronic hepatic insufficiency, cirrhosis, hepatocellular carcinoma, and in the regulated expression of the vanH gene promoter can be used in treatment of Bnterococcus infection, while regulated expression of the androgen receptor gene can be used in the invention to determine the functions of regions within the selected promoters, cancer This sequence represents a primer used in the invention to determine the functions of regions within the selected promoters, New nucleic acid regulatory sequences, which are able to regulate expression of a gene operably linked to a promoter, useful for regulating the expression of transgenes and for treating e.g., cancer and HIF-lalpha, hypoxia-inducible factor-1 alpha, human; antisense; cancer; pre-eclampsia; cytostatic; gynaecological; antiinflammatory; nootropic; Gaps ö 14.5%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 1.2e+02; ive 0; Mismatches 3; Indels Human hypoxia-inducible factor-1 alpha antisense oligo #66. Sequence 16 BP; 2 A; 9 C; 2 G; 3 T; 0 U; 0 Other; Claim 13; Page 60; 95pp; English. AALS6970/c ID AALS6970 standard; DNA; 16 BP. 23 04-APR-2003; 2003WO-IB001758 05-APR-2002; 2002US-0370126P CTGGGAGGTGGAGAGC 1 38 CTGAGAGGTAAAGAGC 11-MAR-2004 (first entry) Query Match
Best Local Similarity 81.2
Matches 13, Conservative immunological diseases. neuroprotective; ss. WO2003085110-A2 Homo sapiens 16-0CT-2003 16 AAL56970; RESULT 150 셤 ઠ ö

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Kristjansen PEG;

WPI; 2003-812728/76 Thrue CA, Hog AM, (CURE-) CUREON AS.

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The present invention relates to compounds capable of modulating hypoxia-
inducible factor-lalpha (HIFIa). The compounds are used to treat patients
with, or at risk of developing, cancer (e.g. of breast, prostate,
pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's
disease, for modulating angiogenesis, proliferation of erythrocytes and
other cells, iron, glucose and energy metabolism, pH regulation, tissue
invasion, apoptosis, multiple daresty metabolism, pH regulation, tissue
and matrix metabolism, especially apoptosis where modulation is
sensitivity to an apoptotic stimulus, particularly a chemotherapeutic
agent and for inhibiting proliferation of cells (especially cancer cells)
in vitro. The present sequence is an antisense oligomuclocide against
HIFlalpha identified in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmacceutical or cosmetic agents for control of skin ageing. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential
                                       oligonucleotide that modulates hypoxia-inducible factor-lalpha, inl for treating e.g. cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                                                                                     Claim 1; Page 42; Opp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HENK ) HENKEL KGAA
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                                                                              useful
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sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss.
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                                                Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
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                                                                                DB 1;
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                                                                                                                                                                                                                                                            ABV71507 standard; cDNA; 11 BP
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                                                                                               Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                         Human skin EST 9293.
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Rest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                         Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-restenosis phosphorothioate oligonucleotide hairpin loop region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 76; 1345pp; German.
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                                                           ABV64086 standard; cDNA; 11 BP.
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                                                                                                                                                                                   Human skin EST 1872.
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The present sequence comprises the 5' or (preferably) 3' terminal hairpin loop region of anti-restenosis phosphorothioate oligomucleotides of the invention (see also ACCS9756-57). A claimed oligomucleotide for treating restenosis, e.g. in smooth muscle tissue, comprises a phosphorothioate modified oligomucleotide that includes at least one hairpin loop, a dr or dG releasing group and at least one multi-guanosine sequence. The oligomucleotide has a long active life in vivo due to the presence of the hairpin loop. It may be used as, or in, a coating on a device for implantation into the body, e.g. a stent for use in percutaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-restenosis agent for treating restenosis e.g. in smooth muscle tissue, comprises a phosphorothioate-modified oligonucleotide comprising one hairpin loop and a dT or dG releasing group.
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/note= "OTHER= phosphorothioate nucleotides"
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86;
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100.0%; Pred. No.
Location/Qualifiers
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The sequence is that of an antisense oligonucleotide which can be used for inhibiting growth or replication of herpesviruses. It corresponds to an antisense sequence of a herpesvirus site, pref. in a gene that is essential for synthesising nucleic acids e.g. the immediate early genes or Vmw65. It can be prepd. by solid phase triester or phosphor-amidite chemistry or by recombinant DNA techniques. It can be used for treating infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2 (HSV-2), varicella zoster (VSV), Betedin-Barr (BBV), cytomegalovirus (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the thibitition of herpesvirus growth or replication may indirectly forestall the progression of events from HIV exposure to the clinical manifestation of AIDS. It may also be useful in the detection, diagnosis and manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
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                                                                                                                                                                                                                                                                                                                                                          New anti:sense oligo:nucleotide(s) for inhibiting HSV - also used for diagnosis and for inhibiting HIV activation by herpes virus.
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Pred. No. 95;
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100.0%; Pred. No. >-.
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91WO-US006646.
                                                                 90US-00586185
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                                                                                                                           (UYMA-) UNIV MARYLAND BALT
(UYJO ) UNIV JOHNS HOPKINS
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18-SEP-1991;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide SEQ ID NO 14594 for detecting SNP TSC0003290.
                                                     Claim 1; SEQ ID NO 320928; 29pp + Sequence Listing; German.
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                  methylation status.
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Set of oligonucleotides, useful for diagnosis and cell typing, is

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Berlin

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Olek A,

WPI; 2001-657177/75

07-APR-2000; 2000DE-01019173

(BPIG-) BPIGENOMICS AG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 84.6%; Pred. No. 1e+02;
Matches 11; Conservative 1; Mismatches 1; Indels
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                                                                                                                           Sequence 13 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 1 Other;
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AGAAGTAAAGAGY 1
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                            Oligonucleotide SEQ ID NO 181997 for detecting SNP TSC0044987.
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ABF82000 standard; DNA; 13
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI0010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 14593; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.3%; Score 11; DB 1; Length 13; 84.6%; Pred. No. 1e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                 Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin K;
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les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABH24940 standard; DNA; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAAGTAAAGAGY 13
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                                                          Piepenbrock C,
(EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI, 2001-657177/75
                                                                                                                        WPI; 2001-657177/75
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                                                              olek A,
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Matches
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ö This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Gaps ö 14.3%; Score 11; DB 1; Length 13; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels Seguence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other; 100.0%; Pred. ... 11; Conservative 51 AGAGGTAAAGA 12 41 AGAGGTAAAGA Best Local Similarity Query Match 163 Matches 

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AAA26129 standard; DNA; 14 BP AAA26129; RESULT 16 AAA26129 

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothhoate; endonuclease; anticancer; breast cancer; endometrium cancer; ss. Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2627.

(first entry)

19-JUL-2000

Homo sapiens W09954459-A2

19-APR-1999; 28-OCT-1999

99WO-US008547.

98US-0082404P. 98US-00103636. 20-APR-1998; 23-JUN-1998;

(RIBO-) RIBOZYME PHARM INC.

Bellon L; Karpeisky A, Haeberli P; Beigelman L, Mcswiggen JA, Zwick M, Jarvis T, Woolf T, Matulic-Adamic J; Thompson JD, Revnolds M,

WPI; 2000-013248/01.

New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer.

Claim 79; Page 99; 148pp; English.

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research

ö reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24147 represent cestrogen receptor hammerhead ribozyme sequences, and AAA24148 to AAA25992 represent their corresponding target sequences, AAAA2593 to AAA26105 represent cestrogen receptor hairpin ribozyme sequences, and AAAA2611 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26217 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present Gaps ö 14.3%; Score 11; DB 1; Length 14; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels Sequence 14 BP; 2 A; 4 C; 7 G; 1 T; 0 U; 0 Other; Local Similarity 100. 9 ACGGCCTGGGG 19 3 Acceccreces 13 invention Query Match Matches 888888888888888 Š

BP. ABT13117 standard; DNA; 14 30-JAN-2003 (first entry) ABT13117; RESULT 164 ABT13117

Cytostatic; dermatological; vasotropic; anti-anaemic; FA pathway defect; Fanconi anaemia protein complex; FANCD; DNA repair; Cockayne's syndrome; cell cycle abnormality; Fanconi anaemia; ataxia telangiectasia; cancer; Bloom's syndrome; Hereditary non-polyposis colon cancer; gene therapy; Fanconi anaemia FANCD intron/exon junction oligo SEQ ID No 20.

02-NOV-2001; 2001WO-US045561. Xeroderma pigmentosum; ds. WO200236761-A2. Unidentified. 10-MAY-2002 

Grompe M; Timmers C, D'andrea AD, Taniguchi T,

(DAND ) DANA FARBER CANCER INST INC.

03-NOV-2000; 2000US-0245756P.

WPI; 2002-519251/55.

Novel isolated Fanconi anemia protein complex polypeptide, termed FANCD2, useful for treating Fanconi anemia pathway defect in cell target or for treating patient with defective FANCD2 gene.

Claim 7; Page 54; 103pp; English.

The invention relates to an isolated Fanconi anaemia protein complex (FANCD2) polypeptide. The FANCD2 protein comprises a sequence of 1472 amino acids fully defined in the specification, its 90% identical sequence, a sequence encoded by a polynucleotide that is at least 90% identical to sequence sylven in specification such as a 5127 base pair sequence, or a fragment which is at least 50 amino acids in length. The FANCD2 protein is useful for treating an FA pathway defect in a cell target or for treating a patient with a defective FANCD2 gene. The FANCD2 protein and its gene are useful as a novel target for therapeutic development, and in diagnostic test and sercening assays for diseases associated with DNA repair and cell cycle abnormalities such as Fanconi anaemia, Bloom's syndrome, Cockayne's syndrome, Hereditary non-polyposis

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Gaps

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Length 15; Indels

DB 1; Leus 3. 1.2e+02; 0;

0; Mismatches

Query Match 14.3%; Score 11; Best Local Similarity 100.0%; Pred. No. Matches 11; Conservative 0; Mismatch

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45 GTAAAGAGCCA 13 GTAAAGAGCCA

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Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

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angioplastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes target specific regions of the CETP gene, they have low nonspecific activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                Gaps
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                                                                                                                     14.3%; Score 11; DB 1; Length 15; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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                                                                                                 Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
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99US-00257608.
99US-00274553.
                                                                                                                                                                                                                                                        AAZ64343 standard; RNA; 15 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                               11; Conservative
                                                                                                                                                                       33 GTCCTCTGAGA 43
                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus
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25-FEB-1999;
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ID AAZ6
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Enzymatic nucleic acid, hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer; autoimmune disease; ss.

Hepatitis C virus. 409955847-A2

Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8123.

AAZ64344 standard; RNA; 15 BP.

RESULT 168

AAZ64344/

28-MAR-2000 (first entry)

AAZ64344;

ô 14.3%; Score 11; DB 1; Length 15; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other; 11; Conservative 45 GTAAAGAGCCA 55 Local Similarity Query Match Best Loca Matches ઠે The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the target these sites and their activities optimised by either varying the carget of the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatitis C virus (HCV) infection, other infectious diseases, autoimmune diseases, and cancer

character nucleic acid, especially a hammerhead ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the Hepatitis C virus (HCV) RNA sequence at the base position given in the Hepatitis C virus (HCV) RNA sequence was screened for optimal ribozyme c arget sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the target these sites and their activities optimised by either varying the rarget these sites and their activities optimised by either varying the rarget these sites and their activities optimised by either varying the nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatocellular carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune diseases, and cancer ö Novel ribozymes for the treatment of diseases and conditions related to Gaps The present sequence represents the preferred target sequence of an Claim 1; Page 89; 123pp; English. hepatitis Cinfection. WPI; 2000-062023/05. 

Claim 1; Page 89; 123pp; English.

Roberts E, Pavco PA, Macejak D;

98US-0083217P. 98US-0100842P. 99US-00257608. 99US-00274553.

(RIBO-) RIBOZYME PHARM INC.

Blatt L, Mcswiggen JA,

99WO-US009027

26-APR-1999; 27-APR-1998; 18-SEP-1998; 23-MAR-1999;

04-NOV-1999

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colon cancer, ataxia telangiectasia and Xeroderma pigmentosum. The FANCD2 gene is useful in producing probes and primers for screening patients in genetic based test, for diagnosing Fanconi anaemia and cancer, for preparing an experimental mouse model for use in screening new in gene therapy methods. A recombinant vector containing the FANCD2 gene of the invention is useful in gene therapy. This polymucleotide sequence represents a FANCD intron/exon junction oligonucleotide relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method of diagnosing or determining if a patient has cancer or is at increased risk of cancer, involving testing a Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a cancer-associated defect, where the presence of one or more cancer-associated defects is indicative of cancer or an increased risk of cancer in the patient. The method of the invention has cytostatic activity. The method is useful for determining if a patient has cancer, or is at increased risk of developing cancer, e.g. breat, ovarian or prostate cancer. A microarray of the invention is useful for determining if a patient has cancer, or is at increased risk of developing cancer, by hybridising a nucleic acid sample to the nucleic acid sequences from the array, and detecting the presence of mutations in RA/BRCA pathway genes in the nucleic acid sample from the patient, where detecting the presence of mutations is indicative of a patient who has cancer, or is at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray; chemosensitising; ds.
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Pred. No. 1.1e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                 Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
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UNIV OREGON HEALTH SCI.
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2001WO-US045561.
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02-NOV-2001;
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Best Local 8
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cerer transfer protein (CERT) hammardened (HH) ribozymes (See AAT99881-
CE TS0137). CETP is a 74 kD glycoprotein that facilitates neutral lipid
cransfer between plasma lipoproteins. The numbering of the targets refers
to the position of the cleavage site in full length CETP. The ribozyme
binds to 5 nucleotides either side of this site, provided the sequence UH
cc is immediately upstream. The ribozymes are able to cleave mRNA from the
gene encoding CETP, thereby blocking synthesis and/or expression of the
mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway
cc an be inhibited (or eliminated) thereby preventing the reduction in size
density of the high density lipoproteins (HDL), prolonging HDL half life,
and therefore increasing HDL levels The ribozymes can be used to treat
conditions associated with abnormal levels of CETP, specifically familial
typercholesterolaemia, atherosoclerosis, peripheral vascular disease,
typercholesterolaemia, hyposlophalipoproteinsemia, dyslipidaemia,
vascular complications of diabetes, transplant, atherectomy and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neurral lipid transfer; plasma lipoprotein; atheroselerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia; peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor; angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
increased risk of developing cancer. A method of the invention is useful
                    for screening a chemosensitising agent, and the agent obtained is useful for treating a patient having a cancer. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial hypercholesterolaemia.
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                                                                                               Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                          1.1e+02;
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                                                                                                                                                  100.0%; Prec. ...
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                                      for treating a patient having a cance
the exemplification of the invention.
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                                                                                                                                                                             Conservative
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Local Sum.
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11 GTAAAGAGCCA
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Wed Apr 19 16:15:55 2006

AAD25954 standard; DNA; 15 BP

AAD25954;

(first entry) 26-MAR-2002 ASO probe #7 to detect human PI4 gene polymorphisms.

PS; haplotyping; genotyping; acute pancreatitis; drug screening; antiinflammatory; chromosome 14q31-q32.1; probe; ss.

Homo sapiens

WO200179227-A2

25-OCT-2001.

13-APR-2001; 2001WO-US012255.

13-APR-2000; 2000US-0196990P

(GENA-) GENAISSANCE PHARM INC

Sanchis A; Choi JY, Koshy B,

WPI; 2002-075060/10.

Genotyping protease inhibitor 4 gene of individual for determining haplotype of individual, involves determining identity of nucleotide pair at specific polymorphic sites for two copies of gene.

Claim 16; Page 13; 79pp; English.

The present invention relates to genotyping procease inhibitor (PI) 4

(kallistatin) gene of an individual, involves determining for the two
copies of the PI4 gene present in the individual, the identity of the
nucleotide pair at one or more polymorphic sites. PI4 gene is located on
chromosome 14q1-q32.1. Genotyping is useful for determining if an
individual has a haplotype or haplotype pairs defined in the
specification. Haplotyping is useful for improving the efficacy and
reliability of several steps in the discovery and development of drugs
for treating diseases associated with PI4 activity, e.g. acute
pancreatitis, to validate PI4 as a candidate agent for treating a
specific condition or disease predicted to be associated with PI4
activity, and in the design of clinical trials of candidate drugs for
treating a specific condition or disease predicted to be associated with
PI4 activity. The PI4 gene is useful in studying the expression and
function of PI4, and in expressing PI4 protein for use in screening for
candidate drugs to treat diseases related to PI4 activity. The present sequence is a ASO (alle PI4 gene polymorphisms 

Sequence 15 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 1 Other;

ö 14.3%; Score 11; DB 1; Length 15; 84.6%; Pred. No. 1.2e+02; tive 1; Mismatches 1; Indels 11; Conservative Local Similarity Query Match Matches

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Gaps

61 GCTGATGTCCTGT 73

ઠે 셤 RESULT 170

ABL88306 standard; DNA; 15 BP. ABL88306/cID ABL88

ABL88306; 

20-MAY-2002 (first entry)

Human CHRNE allele-specific oligonucleotide (ASO) primer, SEQ ID NO:40.

cholinergic receptor nicotinic epsilon polypeptide; CHRNE; Human;

chromosome 17p13-12; acetylcholine receptor; AChR; neuromuscular junction; skeletal muscle; postnatal development; congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype; genetic variant; single nucleotide polymorphism; SNP; gene therapy; drug screening; allele-specific oligonucleotide; ASO; primer; ss.

domo sapiens

WO200198316-A2.

27-DEC-2001.

20-JUN-2001; 2001WO-US019835.

20-JUN-2000; 2000US-0212870P.

(GENA-) GENAISSANCE PHARM INC

Tanguay DA; Koshy B, Kliem SE, Bieglecki KM, Amaro E,

WPI; 2002-130787/17.

Novel genetic variants of cholinergic receptor, nicotinic, epsilon polypeptide gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. congential myasthenic syndrome

Claim 17; Page 14; 104pp; English.

The invention relates to a method for haplotyping the cholinergic receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an individual, and also describes 17 novel polymorphic sites within the human CHRNE gene. The CHRNE gene is located on chromosone 17p13-12 and contains 12 exons which encode a 493 amino acid protein (ABB49112). The CHRNE gene is located on chromosone 17p13-12 and contains 12 exons which encode a 493 amino acid protein (ABB49112). The CHRNE protein is one of the 5 subunits of mammalian acetylcholine acetylcholine acetylcholine acetylcholine acetylcholine receptors (AChRs) found at neuromwascular junctions in juveniles and adults, and is essential for the normal postnatal development of skeletal muscle. Mutations in the CHRNE gene are associated with congenital compact that can be used in gene therapy. The CHRNE gene is also useful for studying the expression and function of CHRNE, and in expressing CHRNE protein for use in correcting for candidate drugs to treat diseases related to CHRNE. The method of the invention is useful for haplotyping the CHRNE gene in an individual, and can also be used in pharmaceutical research to validate candidate drugs for, treating a specific condition drugs or disease confident educes (AERNE activity such as CMS. Polymorphisms in the target region may be determined by the use of allele-specific condidate (ABL88370-ABL88320) as probes and primers, and by primer extension using oligomuclectide primers comprising sequences ABL88371-ABL88331. The charge of several steps in the drug or disease. development of drugs for treating diseases associated with CHRNB activity, and may be used to screen drugs which target CHRNB. Sequences ABL88287-ABL88320 represent specifically claimed allele-specific oligonucloetide (ASO) primers used for detecting polymorphisms in the CHRNE gene

Sequence 15 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 1 Other;

ö Score 11; DB 1; Length 15; Pred. No. 1.2e+02; 1; Mismatches 1; Indels 1; Mismatches . Match Local Similarity 84.6%; 11; Conservative Query Match Matches

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Gaps

33 GTCCTCTGAGAGG 45

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14 KTACTCTGAGAGG 2
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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin of the substrate sequences defined in the specification. The HCV is the substrate sequences defined in the specification. The HCV is the substrate sequences defined in the specification. The HCV is the substrate sequences defined in the specification. The HCV is they can be used to treat cirrhosis, liver failure and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or reating a condition associated with HCV infection in conjunction with one or more contert drug therapies, particularly type I interferon, especially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: Some of the sequence data for this patent was printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                     Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme, HCV expression, HCV replication, cirrhosis, virucide, liver failure, hepatocellular carcinoma, HCV infection, drug therapy, type I interferon, interferon alpha, interferon beta, cytostatic; interferon gamma, consensus interferon, hepatotropic, antiinflammatory, substrate, hammerhead ribozyme, HH ribozyme, ss.
                                                                                                                                                                                                                                                                                                   Hepatitis C virus substrate #1178 for HCV hammerhead ribozyme #1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roberts B, Pavco PA, Macejack D;
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                                                                         BP.
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                                                                         ABX01396 standard; RNA; 15
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MCSWIGGEN J A.
ROBERTS B.
PAVCO P A.
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(ROBE/)
(PAVC/)
RESULT 171
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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The carzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV itbozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirthosis, liver failure and/or replication of hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon, especially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                          Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection; HCV ribosyme; HCV expression; HCV replication; cirrhosis; virucide; liver failure; hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss.
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                                                                                                                                                       Hepatitis C virus substrate #1179 for HCV hammerhead ribozyme #1179.
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14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                   ABX01397 standard; RNA; 15 BP.
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                                                                                                                 23-DEC-2002 (first entry)
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ROBERTS B.
PAVCO P A.
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                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
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                                                                           ABX01397;
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(MACE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROBE/)
RESULT 172
                  ABX01397,
                                                          %XCCCCCCCCCCCCCCCX8X4444X8X1X3334X4X4X6X4X8X8X8X8X8X8X8X8X8X8X
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RESULT 173

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Gaps

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0; Indels

14.3%; Score 11; DB 1; Length 15; 100.0%; Pred. No. 1.2e+02;

100.0%; Pred. No.

11; Conservative

Best Local Similarity

Matches

Query Match

GTAAAGAGCCA 55

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13 GTAAAGAGCCA

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comprising the novel enzymatic nucleic acid; (2) an ammalian cell including the novel enzymatic nucleic acid; (3) an expression vector comprising a nucleic acid sequence encoding at least one enzymatic comprising a nucleic acid sequence encoding at least one enzymatic comprising a nucleic acid sequence encoding at least one enzymatic comprising a nucleic acid sequence encoding at least one fit at mammalian cell including an expression of that concluding an expression of that comprising controlle, (4) a mammalian cell including an expression vector of (3); (6) a method of treating a patient having a condition associated with HCV infection, by contacting cells of the patient with the nucleic acid molecule, and further employing one or more drug therapies; (7) a method for inhibiting HCV replication in a mammalian cell by administering the novel enzymatic nucleic acid; and (8) a method of cell by administering the expression and/or replication of hepatitis C nucleic acid with the separate RNA molecule. The enzymatic nucleic acid is useful for modulating the expression and/or replication of hepatitis C nucleic acid may also be used to treat or prevent the occurrence of a disease state in a patient. The present sequence represents an HCV and a patient. The present sequence represents an HCV and a patient. The present sequence represents an HCV and a patient. The present sequence represents an HCV and a patient. The present sequence represents an HCV and a patient sequence represents and the present and present sequence which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an enzymatic nucleic acid molecule which specifically cleaves minus strand RNA derived from hepatitis C virus HCV). The binding arms of the molecule comprise ribozyme sequences. The molecule is selected from inozyme, G-cleaver, DNAzyme, Amberzyme, and Zinzyme motifs. Also described: (1) a pharmaceutical composition.
                                                                                                                                                                                                                     ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection; antiviral; gene therapy; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New enzymatic nucleic acid molecule, which specifically cleaves minus strand RNA derived from hepatitis C virus, useful for modulating the expression and/or replication of hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pavo PA, Macejack D;
                                                                                                                                                                            Hepatitis C virus hammerhead ribozyme substrate sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3xample 1, Page 40; 65pp; English.
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Length 15; Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other; exemplification of the present invention Query Match

Gaps ö 0; Indels 14.3%; Score 11; DB 1; Le 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; 11; Conservative 45 GTAAAGAGCCA 55 13 GTAAAGAGCCA 3 Local Similarity Matches

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ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection; antiviral; gene therapy; substrate; ss. New enzymatic nucleic acid molecule, which specifically cleaves minus strand RNA derived from hepatitis C virus, useful for modulating the expression and/or replication of hepatitis C virus. Roberts E, Pavo PA, Macejack D; Hepatitis C virus hammerhead ribozyme substrate seguence. Example 1; Page 40; 65pp; English. 15-PEB-2000; 2000US-00504231. 99US-00274553. AEB76105 standard; RNA; 15 (first entry) Blatt L, Mcswiggen JA, BLATT L. MCSWIGGEN J A. WPI; 2002-215899/27. (PAVO/) PAVO P A. (MACE/) MACEJACK D. ROBERTS B. Hepatitis C virus. US2002013458-A1. 23-MAR-1999; 22-SEP-2005 31-JAN-2002 ABB76105; (ROBE/) (PAVO/) (BLAT/) (MCSM/) RESULT 174 AEB76105/ 

The invention relates to an enzymatic nucleic acid molecule which specifically cleaves minus strand RNA derived from hepatitis C virus (HCV). The binding arms of the molecule comprise tibozyme sequences. The molecule is selected from inozyme, G-cleaver, DNAzyme, Amberzyme, and C zinzyme motifs. Also described: (1) a pharmaceutical composition comprising the novel enzymatic nucleic acid; (2) a mammalian cell including the novel enzymatic nucleic acid; (3) an expression vector comprising a nucleic acid sequence encoding at least one enzymatic nucleic acid molecule, (4) a mammalian call including at least one enzymatic molecule; (4) a mammalian call including an expression vector of (3); (5) methods for treating co patient the novel enzymatic nucleic acid or the vector of (3); (6) a method of treating a patient having a condition associated with HCV infection, by contacting cells of the patient with cell manufacting the novel enzymatic nucleic acid or the novel enzymatic nucleic acid and contacting the novel enzymatic nucleic acid and contacting the novel enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid with the separate sequence represents an HCV winns strand. The nucleic acid may also be used to treat or prevent the occurrence of a disease state in a patient. The present sequence repre exemplification of the present invention

Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

ö Gaps .. 0 14.3%; Score 11; DB 1; Length 15; 100.0%; Pred. No. 1.2e+02; Indels ö Best Local Similarity 100.0%; Pred. No. 1.2 Matches 11; Conservative 0; Mismatches Query Match

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nb DT, Chowrira B, Direnzo A, Draper Ku, Luuyu ...., Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                  gene expression; downregulator, interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozymes having modified bases and methods for producing them - for use
                                                                                                                                                                  Mouse IL-5 hammerhead ribozyme target sequence (nt. position 36)
                                                                                                                                                                                         Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00227958.
94US-00228041.
94US-00245736.
94US-00291932.
94US-00291873.
94US-00291873.
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94US-00303039.
94US-00311486.
                                                                               AAT54540 standard; RNA; 15 BP
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94US-00222795.
94US-00224483.
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94US-00319492
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94US-00345516
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                                                                                                                                            (first entry)
45 GTAAAGAGCCA 55
               GTAAAGAGCCA 1
                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1994;
15-APR-1994;
18-MAY-1994;
                                                                                                                              25-MAR-2003
22-APR-1997
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07-OCT-1994;
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04-NOV-1994
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Modak A,
                                                                                                        AAT54540;
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-5) mRNA at the nucleotide base position indicated in the DE line. Regions to the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the IL-5 target sequences and thereby inhibit IL-5 expression, making them useful for treating chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes and preventing the recruitment and activation of eosinophils. The ribozymes can also be used to treat cosinophilia (related to parasitic infection or with pulmonary infiltration) and L-tryptophan-associated cosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chromic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawaaski disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse IL-5 hammerhead ribozyme target sequence (nt. position 36)
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                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02; ive 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
in inhibiting disease related genes.
                                   Claim 2; Page 220; 407pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT54538 standard; RNA; 15 BP.
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94US-00218934.
94US-00222795.
94US-00227958.
94US-00227958.
94US-00271280.
94US-00291433.
94US-00291433.
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                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.7
Matches 12; Conservative
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22-APR-1997 (first en
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16-AUG-1994;
17-AUG-1994;
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04-APR-1994
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AAT54538/c
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                                                                                                                                                                                                                           Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA; Modak A, Pavco P, Bejgleman L, Sullivan SM, Sweedler D, Thompson JD; Tracz D, Usman N, Wincott FB, Woolf T;
                                                                                                                                                                                                                                                                                                                  Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02; 1.ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
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94US-00293520.
94US-00300000.
94US-00311486.
94US-00311749.
94US-0031671.
94US-00319492.
94US-00319492.
94US-00337608.
94US-00337608.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                        08-SEP-1994,
23-SEP-1994,
28-SEP-1994,
28-SEP-1994,
03-OCT-1994,
11-OCT-1994,
11-OCT-1994,
11-OCT-1994,
28-NOV-1994,
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21-APR-1997
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IID AAT5
XX AC AAT5
XX XX Z5-M
DT 25-M
XX X1-21-A
XX XX Enzy
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Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; theumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
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940S-0022795
940S-0022795
940S-00228041
940S-0021536
940S-0029132
940S-00291433
940S-00291433
940S-00291433
940S-00391433
940S-00311486
940S-0031149
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                                                                                                                                                   WO9523225-A2
                                                                                                                  Homo sapiens
                                                                                                                                                                                                                  23-FEB-1995;
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07-OCT-1994;
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23-SEP-1994;
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o DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Bavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincete FB, Woolf T; Stinchcomb DT, Modak A, Tracz D, Grimm S,

(RIBO-) RIBOZYME PHARM INC.

## WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them - for in inhibiting disease related genes.

## Claim 2; Page 229; 407pp; English.

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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DB line. The relA gene product is a subunit of the transcriptional regulator NP-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and halrpin ribozyme eleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave their capteneds and thereby inhibit relA expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential and that uses are limited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)

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15 CCAAGATGATGTCC 2

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                                                                                                                                                                                                                                                                         cleavage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                                                                                                                 Substrate for HH ribozyme HCV-3329 which cleaves HCV RNA at nt. 3329.
                                                     Gaps
                                                                                                                                                                                                                                                                        Enzymatic nucleic acid, hammerhead ribozyme; virus replication; cirrhosis; liver failure; hepatocellular carcinoma; interferon; autoimmune disease; ss.
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                         14.0%; Score 10.8; DB 1; Length 15; 64.3%; Pred. No. 1.3e+02; Live 3; Mismatches 2; Indels
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Sequence 15 BP; 4 A; 3 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blatt L, Mcswiggen JA, Roberts E, Pavco PA,
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98US-0100842P.
99US-00257608.
99US-00274553.
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Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                     AAZ62575 standard; RNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC.
                                                                              29 TGGAGTCCTCTGAG 42
                                                                                             UGGAGUACCCUGAG 15
                                                                                                                                                                                                                         (first entry)
                                     Local Similarity 64.3
nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                           Hepatitis C virus.
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25-FEB-1999;
23-MAR-1999;
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                                                                                                                                                                                               AAZ62575;
                            Query Match
                                                                                                                                            Matches
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The invention relates to the isolation of sequences encoding human haemopoietin receptor protein family NR8 genes. The NR8 family sequences were initially searched for comparison on a nucleic acid database with the nucleic acid probe sequence TGABGYNNNTGABGY encoding the amino acid sequence Trp-Ser. The sequences AAZ59258-Z59300 and AA290816-280925 expresent specific examples of probe sequences used in the search. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                                                                                                                                                                                                                                                    Haemopoietin receptor family, NR8; antibody; diagnos
blood formation disorder; fusion protein; probe; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used for the treatment of such disorders
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                                                 ВP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA63392 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-JP003351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-00214720
98JP-00297409
                                                 AAZ90853 standard; DNA; 15
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                                                                                                                                                  (first entry)
                                                                                                                                                                                                    Human NR8 gene probe #81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nomura H, Maeda M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               WO9967290-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-OCT-1998;
                                                                                                                                                  24-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1999
                                                                                                   AAZ90853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA63392;
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Matches
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RESULT 179
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ID AAA6:
XX AC AAA6:
XX DT 06-M
XX C-10'
XX C-10'
XX C-10'
XX Ened
XW Ened
XW Ened
XW Ened
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57 CGAAGCTGATGTCC 70

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention is concerned with the elucidation of the gene cluster from Streptomyces globisporus which regulates enediyne C-1027 synthesis. Enediyne C-1027 is an antibiotic, consisting of an apoprotein and a non-peptidic chromophore, which causes damage to DNA. The primers AAA63353-A63451 were used to isolate the open reading frames which used the gene cluster. The sequences within the gene cluster can be used to produce the protein and to identify antagonists, both of which can be used in the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid comprising a nucleic acid encoding any of C-1027 open reading frames (ORFs) -7 to 42, excluding ORF 9 (cagA), useful for the production of enediyne C-1027 antitumor antibiotics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 3 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 Standage S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 17; 160pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                             Shen B, Liu W, Christenson SD,
                                                                                                                                                                                                                        06-JAN-1999; 99US-0115434P.
                                                                                                                                                              06-JAN-2000; 2000WO-US000446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AACAAGACGGCCTG 16
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Matches 12; Conserv
                              WO200040596-A1.
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                                                                                            13-JUL-2000
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AME 19914
AME 199
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-like Growth Factor [IGR]-1.

Teceptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of infibiting or reducing growth factor mediated cell proliferation, clipmunation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense of infibiting or rectide is used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153-CPF5161). The method is useful for ameliorating the effects of psoriasis, inchtyposis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, seleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
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                                                                           Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 BP; 4 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
  Edmondson SR
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                                                                                                                                                                          Example 8; Page 65; 201pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vessels or any other hyperplasia
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Best Local Similarity 85.7
Matches 12; Conservative
  Werther GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Werther GA,
                                      WPI; 2001-041421/05.
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                                                                                                                                       inflammation.
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Wraight CJ,
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vessels or any other hyperplasia 21-JUN-2000; 2000WO-AU000693. IGF-I oligonucleotide #775. 21-JUN-1999; 28-DEC-2000 AAF49815; 33 RESULT 183 셤

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperproliferation of the retina, brain or skin, growth factor-mediated mainsancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or Example 8; Page 84; 201pp; English. Ameliorating the UV (ultra...' inflammation.

Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

ch 14.0%; Score 10.8; DB 1; Length 15; I Similarity 85.7%; Pred. No. 1.3e+02; 12; Conservative 0; Mismatches 2; Indels GTCCTCTGAGAGGT 46 Query Match Best Local Similarity

GTCCTCTGGGAGAT 15

AAF49815 standard; DNA; 15 30-MAR-2001 (first entry)

BP

Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding procein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatoosis, neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasis; kidney disease; neobascular condition; hyperplasis; kidney disease;

Homo sapiens

WO200078341-A1.

(MURD-) MURDOCH CHILDRENS RES INST. 99US-0140345P.

Edmondson SR; Wraight CJ, Werther GA,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering V (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

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                                                           The present invention relates to a method for ameliorating the effects of akin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]—1 receptor, IGF binding protein [IGFBP]—2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153—78151.) The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 4 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
                        Example 8; Page 66; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    vessels or any other hyperplasia
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13 Similarity 85.7%;
12; Conservative
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Best Local Similarity
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Matches
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Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor. I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keardosis; neoplasia; sclaroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neobarchoe the retina; ss. IGFBP3 oligonucleotide #139. 

BP.

AAF46719/c ID AAF46719 standard; DNA; 15

RESULT 184

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Gaps ö

AAF46719;

30-MAR-2001 (first entry)

Homo sapiens.

WO200078341-A1.

28-DEC-2000

21-JUN-2000; 2000WO-AU000693

99US-0140345P 21-JUN-1999;

Werther GA, Edmondson SR; (MURD-) MURDOCH CHILDRENS RES INST. Wraight CJ,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 45; 201pp; English.

The present invention relates to a method for ameliorating the effects of

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skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153-F55161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasis, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF46720 standard; DNA; 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AGAGCCAGCGAAGC
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Ameliorating the effects of a disorder, e.g. psoriasis, by administering JV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

Edmondson SR;

Wraight CJ, Werther GA,

WPI; 2001-041421/05.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonorelectide, (for Insulin-IRA Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation,

Example 7; Page 45; 201pp; English.

inflammation.

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inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; kearsolsis; neoplasia; selaroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
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                                                                                                                                                                                                                                                                       14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.38+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                              Sequence 15 BP; 1 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                          vessels or any other hyperplasia
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                                                                                                                                                                                                                                                                                          Local Similarity 85.7 les 12; Conservative
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Matches
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neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
888888888
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Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Gaps ö 14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02; cive 0; Mismatches 2; Indels 67 CAGCGCTGCTGATG 15 12; Conservative CAGCGAAGCTGATG Query Match Best Local Similarity 54 Matches a 8

AAF52686 standard; DNA; 15 (first entry) 30-MAR-2001 AAF52686; RESULT 187

BP

Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding proctein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasis, kidney disease; neovascular condition of the retina; ss. IGF-I oligonucleotide #3646.

Homo sapiens.

WO200078341-A1

28-DEC-2000.

21-JUN-2000; 2000WO-AU000693

21-JUN-1999;

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Wraight CJ, Werther GA,

WPI; 2001-041421/05

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 84; 201pp; English.

skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasiss, cleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic The present invention relates to a method for ameliorating the effects of AAP52666

MAP52666

MAP52666

MAP5AAP5

MAP5AA

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disease, kidney disease, hyperproliferation of the inside of blood
                                                                                                   Length 15;
                                                             Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other
                         vessels or any other hyperplasia
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Indels Score 10.8; DB 1; Pred. No. 1.3e+02; 0; Mismatches 2; Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative

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Gaps

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33 GTCCTCTGAGAGGT 46 Н ò 셤

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RESULT 188 AAF50644,

BP. AAF50644 standard; DNA; 15

AAF50644;

(first entry) 30-MAR-2001

IGF-I oligonucleotide #1604.

cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; the retina; ss. Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

Homo sapiens.

WO200078341-A1

28-DEC-2000

21-JUN-2000; 2000WO-AU000693

99US-0140345P 21-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Wraight CJ,

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

Example 8; Page 71; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGFP-1] receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation.

CC oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAP45151 and AAP45153-CP F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, chthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, bypernecvascular condition such as a necvascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood or any other hyperplasia vessels

Sequence 15 BP; 3 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

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Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityrissis; IGF binding procein; IGFBP-2; IGFBP3; inflammation; psoriasis; piratis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; Keatosis; neophasia; scleroderma; wart; skin cancer; sclerotic disease; hypermeovascular condition; hyperplasia; kidney disease; neovascular condition; freina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for ameliorating the effects of anti disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pitaris, serborrhoea, keloids, keratosis, ineoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition ouch as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, hyperproliferation of the inside of blood
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                                        Gaps
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Score 10.8; DB 1; Length 15;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
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  14.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                               IGF-I oligonucleotide #2989
                                                                          54 CAGCGAAGCTGATG 67
                                                                                                                                                                                                              AAF52029 standard; DNA; 15
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                 CGGTGAAGCTGATG 2
                  Similarity 85.7
12; Conservative
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  Query Match
Best Local &
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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      akin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGF]-1, which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAP45151 and AAF45153-F45161). The method is useful for amaliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ichthyosis, pityriasis, varts, benign growths, cancers of the skin, a hyperneovascular condition of as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to a method for ameliorating the effects of
                                                                                                                                                                                                                                                                                      Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SR;
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                                                                                                                                                                                                                                                    IGP-I oligonucleotide #1605.
  68
                                    14
                                                                                                                                   AAF50645 standard; DNA; 15
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                                      1 AGCGCTGCTGATGT
  AGCGAAGCTGATGT
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22
                                                                                                                                                                         AAF50645;
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Indels

14.0%; Score 10.8; DB 1; Length 15; larity 85.7%; Pred. No. 1.3e+02; Conservative 0; Mismatches 2; Indels

Local Similarity les 12; Conserv

Best Loc Matches

Query Match

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Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; innzyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease; diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (FTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (FKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HRB2/), cerb2/neu), phospholaman (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes tinclude hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinclude hammerhead (HH), hairpin, nCH (inozyme), d-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Ch
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                              Human anti-HER2 NCH ribozyme substrate sequence #954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 491; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0151713P.
99US-00406643.
99US-0156236P.
99US-0156467P.
99US-00436430.
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99US-0173612P.
99US-00476387.
                                    ADV37122 standard; RNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-00498824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-00531025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            obesity and heart disease.
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-244406/25.
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200116312-A2.
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Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
29-DEC-1999;
30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2000;
                                                                                                            10-FEB-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999
                                                                       ADV37122;
RESULT 191
               ADV37122,
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diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for an anti-HER2 NCH riboxyme used in the examples of the present invention. Note: Some SRQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them. protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; https://dx.discommerce.com/phai.pKC alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PKI; presentiln-1; ps-1; presentiln-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme; zinzyme; cancer; breast cancer; Alzheimer's disease; disbetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human; Enzymatic nucleic acid molecules able to cleave separate RNA molecules Gaps Ë, Enzymatic nucleic acid molecule; gene expression; down regulation; Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Chowrira Beaudry A, Zinnen S, Lugwig J, Sproat BS; ö Score 10.8; DB 1; Length 15; Pred. No. 1.3e+02; 0; Mismatches 2; Indels Human anti-HER2 NCH ribozyme substrate sequence #168. Sequence 15 BP; 5 A; 5 C; 4 G; 0 T; 1 U; 0 Other; ADV35537 standard; RNA; 15 BP 990S-00406643. 990S-0156236P. 990S-0156467P. 990S-0169100P. 990S-017432. 990S-017432. 2000US-00498824. 2000US-00531025. 2000US-0197769P. 2000US-00578223. 14.0%; 85.7%; 30-AUG-2000; 2000WO-US023998 2000US-00636385 (RIBO-) RIBOZYMB PHARM INC 25 ACTCTGGAGTCCTC 38 10-FEB-2005 (first entry) 14 Acreresecretre 1 Local Similarity 85.7 nes 12; Conservative Mcswiggen J, Usman N, WPI; 2001-244406/25. WO200116312-A2 À Homo sapiens. 29-DEC-1999; 29-DEC-1999; 30-DEC-1999; 20-MAR-2000; 14-APR-2000; 04-FEB-2000; 09-AUG-2000; Karpeisky A, Stinchcomb D 31-AUG-1999 08-NOV-1999 06-DEC-1999 23-MAY-2000 08-MAR-2001 27-SEP-1999 27-SEP-1999 27-SEP-1999 ADV35537; Query Match RESULT 192 Matches 8888888888 셤 ઠે

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The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase.lb (PTB-1B), methionine alpha (PKC alpha), beta-secretase (BTRRT), protein kinase C alpha (PKZ)-erbZ/neu), phospholamban epidermal growth factor receptor-2 (HRRZ/C-erbZ/neu), phospholamban (PLM), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, MCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present colls are repeated more than once in the specification, but these have
are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 1 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      different sequences associated with them.
                                                                                   Example 7; Page 474; 717pp; English.
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Gaps ö 14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02; 2; Indels 0; Mismatches Query Match
Best Local Similarity 85.79
Watches 12; Conservative

15 ACGCCAGGCCATA 2 셤 ሯ

(first entry) 10-PBB-2005

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase; protein-tyrosine-phosphatase; hTERT; protein kinase Calpha; PKC alpha; beta-secretase; BACE; human epidermal growth factor receptor-2; HERZ; c-erb2; neu; phospholamban; PLN; presentiin-1; ps-1; presentiin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inoxyme; G-cleaver; amberzyme; zinzyme; DNAzyme; cancer; barrain; disease; disease; disease; disease; besity; cardiac disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

Homo sapiens

#O200116312-A2

27-SEP-1999

9 ACGGCCTGGGGATA 22

ö

ADV37121 standard; RNA; 15 ADV37121; RESULT 193 

Human anti-HER2 NCH ribozyme substrate sequence #953.

08-MAR-2001

2000WO-US023998 30-AUG-2000;

99US-0151713P. 99US-00406643. 99US-0156236P. 99US-0156467P. 99US-00436430. 27-SBP-1999; 08-NOV-1999; 06-DEC-1999;

99US-0173612P. 99US-00476387. 2000US-00498824. 2000US-00531025. 2000US-0197769P. 20-MAR-2000; 14-APR-2000; 30-DEC-1999; 04-FEB-2000; 

(RIBO-) RIBOZYME PHARM INC.

09-AUG-2000; 2000US-00636385

Usman N, Blatt L, Beigelman L, Burgin A; Matulic-Adamic J, Sweedler D, Draper K, Chowrira B; Beaudry A, Zinnen S, Lugwig J, Sproat BS; Stinchcomb D, Mcswiggen J, Karpeisky A,

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 7; Page 491; 717pp; English.

molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aninopeptidase (MetAP-2), human tejomerase (HTBRT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HERZ/c-erb2/neu), phospholamban (PLM), presenilin-1 (ps-1), presentilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diseases, hepatitis B infections, and hepatitis and hepatocellular cardinoma. The enzymatic nucleic acid molecules can also be used as disagnostic tools to examine genetic drift and mutations within diseased calls and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for an anti-HBR2 NCH SEQ ID ribozyme used in the examples of the present invention. Note: Some Si Nos are repeated more than once in the specification, but these have present invention relates to the use of enzymatic nucleic acid different seguences associated with them.

Sequence 15 BP; 4 A; 5 C; 4 G; 0 T; 2 U; 0 Other;

Gaps ö Query Match
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels

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셤 ò

RESULT 194

Human anti-HER2 NCH ribozyme substrate sequence #169.

Enzymatic nucleic acid molecule; gene expression; down regulation; protein-tyrosine-phosphatase-lb; PTB-1B; methionine aminopeptidase; MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha; beta-secretase; BACB; human epidermal growth factor receptor-2; HER2; c-erb2; neu; phospholamban; PKI; presenilin-1; ps-1; presenilin-2; ps-2; hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver; amberzyme, zinzyme; DNAzyme, cancer; breast cancer, Alzheimer's disease; 

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diabetes; obesity; cardiac disease; heart disease; age-related disease; hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
                                                                                                                                                                                                                                        Usman N, Blatt L, Beigelman L, Burgin A;
Matulic-Adamic J, Sweedler D, Draper K, Chowrira
Beaudry A, Zinnen S, Lugwig J, Sproat BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      different sequences associated with them.
                                                                                                                                                                                                                                                                                                                       Example 7; Page 474; 717pp; English.
                                                                                                                                                                                                                                                Matulic-Adamic J,
                                                                                                                        99US-0156467P.
99US-00436430.
99US-0169100P.
99US-00474432.
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99US-00476387.
2000US-00498824.
                                                                                                        99US-00406643
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                                                                                 2000WO-US023998
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                                                                                                                                                                                                                                         Usman N,
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                                                                                                                                                                                                                                        Mcswiggen J, U
Karpeisky A, M
Stinchcomb D,
                                                 40200116312-A2
                                                                                                                        27-SEP-1999;
08-NOV-1999;
06-DEC-1999;
29-DEC-1999;
30-DEC-1999;
04-FEB-2000;
                                                                                 30-AUG-2000;
                                  Homo sapiens
                                                                                                                                                                                 20-MAR-2000;
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                                                                                                                                                                                                         09-AUG-2000;
                                                                 08-MAR-2001
                                                                                                                  27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Novel isolated polymorphic variant polynucleotide of lecithin-cholesterol acyltransferase gene, useful for studying expression and biological function of the gene, and for therapeutic, diagnostic or forensic

Chew A, Denton RR, Nandabalan K, Stephens JC;

WPI; 2002-557737/59.

'n

(GENA-) GENAISSANCE PHARM INC.

03-JAN-2001; 2001WO-US000092. 03-JAN-2001; 2001WO-US000092.

WO200253575-A1. Homo sapiens.

11-JUL-2002

Lecithin-cholesterol acyltransferase, LCAT; Norum disease; gene therapy; fish-eye disease; atherosclerotic cardiovascular disease; forensic; population diversity; anthropological lineage; paternity testing; human; polymorphism; allele-specific oligonucleotide; ASO; probe; ss.

Human LCAT gene polymorphism detection ASO probe #2.

(first entry)

07-0CT-2002

ABK97479;

ABK97479 standard; DNA; 15 BP.

ABK97479

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Claim 16; Page 16; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 GCCAGCGAAGCTGA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GACAGCTAAGCTGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   purposes.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-lb (PTB-1B), methionine aminopeptidase (MetAP-2), human telomerase (HTBRT), protein kinase C alpha (FKC alpha), beta-secretase (BACB), human epidermal growth factor receptor-2 (HER2/c-erbZ/neu), phospholamban (PLM), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motifs. The methods of the invention are useful cor treating cancer, in particular breast cancer, Alzheimer's disease, disease, disease, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diseased; calcinoma. The enzymatic nucleic acid molecules can also be used as disagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrace/target sequence for an anti-HERZ ORCH ribozyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes obesity and heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 1 A; 5 C; 5 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ACGGCCTGGGGATA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ACGGCCAGGCCATA 1
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Matches

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The present invention relates to a new polynucleotide comprising a nucleotide sequence which is a polymorphic variant of a reference sequence for lecithin-cholesterol acyltransferase (LCAT). The invention is useful for identifying an association between a trait (preferably a clinical response to drug targeting LCAT) and at least one genotype or haplotype of LCAT gene. The method of the invention has applicability in developing diagnostic tests and therapeutic treatments for Norum disease, fish-eye disease and atherosclerotic cardiovascular disease. The haplotyping and genotyping methods are useful for studying population diversity, anthropological lineage, the significance of diversity and lineage at the phenotypic level, paternity testing, forensic applications crait such as level of drug response or usceptibility to disease. In addition, the methods for identifying the LCAT haplotypes present in addition, the methods for identifying the LCAT haplotypes present in campit the frequency of individual LCAT haplotypes in a population with a specific disease, e.g. Norum disease, will facilitate the development of drugs targeting the LCAT isoform(s) that are most the development of drugs targeting the LCAT isoform(s) that are most treatment in that disease population. The present nucleic acid sequence represents one of a collection (ARSO4748-ARSO49491) of allele-specific oligonucleotide (ASO) probes that were used in the invention to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
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glycosyltransferase 1 (UGT1A1) allele-specific oligonucleotide #31.
                                                                                                                                                                                                                                     Genotyping a human UDP glycosyltransferase 1 gene of an individual for determining the haplotype of an individual, involves determining the identity of a nucleotide pair at specific polymorphic sites for two copies of the gene.
                                                               UDP glycosyltransferase 1; UGTLA1; human; haplotyping; 88; drug discovery; Gilbert's syndrome; Crigler-Najjar syndrome; allele-specific oligonucleotide.
                                                                                                                                                                                                     Rounds E;
                                                                                                                                                                                                                                                                               Claim 16; Page 13; 81pp; English.
AAS99164 standard; DNA; 15 BP
                                                                                                                                                                                    (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                   13-APR-2001; 2001WO-US012273.
                                                                                                                                                                    18-APR-2000; 2000US-0197514P.
                                                                                                                                                                                                     Choi JY, Koshy B,
                                (first entry)
                                                                                                                                                                                                                     WPI; 2002-075063/10.
                                                                                                                  WO200179230-A2.
                                                                                                   Homo sapiens
                                12-MAR-2002
                                                                                                                                   25-OCT-2001.
               AAS99164;
                                                                                                                                                                                                      Chew A,
                                                 ğ
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The invention relates to genotyping a human UDP glycosyltransferase

(UGTIA1) gene of an individual, involving determining for the two copies

(UGTIA1) gene present in the individual, the identity of the

nucleotide pair at one or more polymorphic sites. The new method is

useful for determining whether an individual has a haplotype or haplotype

pairs, given in the specification. It is useful for improving the

efficacy and reliability of several steps in the discovery and

development of drugs for treating diseases associated with UGTIA1

activity, e.g., Gilbert's syndrome and Crigler-Najjar syndrome, to

validate UGTIA1 as a candidate agent for treating a specific condition or disease predicted to be associated with UGTIA1 activity. The

design of clinical trials of candidate drugs for treating a specific

condition or disease predicted to be associated with UGTIA1 activity. The

method is useful to screen for compounds targeting UGTIA1 to treat a

specific condition or disease associated with UGTIA1 activity. A nucleic

acid (I) comprising a polymorphic variant of a reference sequence for the

UGTIA1 gene or CDNA (II) or itsefunded to useful in studying the

expression and function of UGTIA1, and in expressing UGTIA1 protein for

use in screening for candidate drugs to treat diseases related to UGTIA1

cactivity. (I) or (II) is useful for treating and testing of drugs

the UGTIA1 isogenes in vivo, for in vivo screening and testing of drugs

the UGTIA1 isogenes in vivo, for in vivo screening and testing of trugs

the ugrapeutic agents and compounds for testing the efficacy of

therapeutic agents and compounds for testing the efficacy of

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Cargivity of the ugrapeutic agents and compounds for testing the approach of the pages in the ugrapeutic agents and compou
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                                14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02; tive 0; Mismatches 2; Indels
Sequence 15 BP; 3 A; 5 C; 4 G; 2 T; 0 U; 1 Other;
                                                    Local Similarity 85.7
nes 12; Conservative
                                   Query Match
                                                                         Matches
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15 CRGGGGTCCTCTGA 2

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Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection; HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide; liver failure; hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; 88.
                                                           Hepatitis C virus substrate #208 for HCV hammerhead ribozyme #208.
              ABX00426 standard; RNA; 15 BP
                                            23-DEC-2002 (first entry)
                                                                                                                                Hepatitis C virus.
                             ABX00426;
RESULT 197
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US2002082225-A1. 27-JUN-2002

99US-00274553 23-MAR-1999; 99US-00274553

23-MAR-1999;

MCSWIGGEN J A. MACEJACK D. ROBERTS B. PAVCO P A. (ROBB/) (PAVC/) (MACB/) (BLAT/)

Roberts B, Pavco PA, Macejack D; Mcswiggen JA, Blatt L,

WPI; 2002-617759/66.

New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.

Claim 1; Page 27; 80pp; English.

The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprises sequences complementary to one of the substrate sequences defined in the specification. The HCV incompasses are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhozymes are used useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon. The present sequence appears a substrate for a HCV hammerhead (HH) ribozyme. Note: some of the sequence data for this patent was printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html

Sequence 15 BP; 3 A; 3 C; 5 G; 0 T; 4 U; 0 Other;

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Score 10.8; DB 1; Length 15;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels
   ch 14.0%;
1 Similarity 85.7%;
12; Conservative
                    Local Similarity
     Query Match
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Gaps

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57 CGAAGCTGATGTCC 70 | ||| ||||||| 15 CCAAGATGATGTCC 2

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4

28 CTGGAGTCCTCTGA 41

15 CCAAGATGATGTCC

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The invention relates to an enzymatic nucleic acid molecule which specifically cleaves minus strand RNA derived from hepatitis C virus (HCV). The binding arms of the molecule comprise ribozyme sequences. The molecule is selected from inozyme, (2-cleaver, DNAzyme, Amberzyme, and comprising the novel enzymatic nucleic acid; (2) a mammalian cell including the novel enzymatic nucleic acid; (3) an expression vector comprising a nucleic acid sequence encoding at least one enzymatic nucleic acid molecule, in a manner, which allows expression of that comprising a nucleic acid sequence encoding at least one enzymatic molecule; (4) a mammalian cell including an expression of that comprising a nucleic acid molecule, in a manner, which allows expression of that carcinoma by administering to a patient the novel enzymatic nucleic acid or the vector of (3); (6) a method of treating a patient having a condition associated with HCV infection, by contacting cells of the patient with the nucleic acid molecule, and further employing one or more drug cherapies; (7) a method for inhibiting HCV replication in a mammalian cell by administering the novel enzymatic nucleic acid with the separate RNA molecule by contacting the novel enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid is useful for modulating the expression of HCV minus strand. The nucleic acid may also be used to treat or prevent the occurrence of a nucleic acid may also be used to treat or prevent the occurrence of a
                                                                                                                                                                                                   ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection; antiviral; gene therapy; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New enzymatic nucleic acid molecule, which specifically cleaves minus strand RNA derived from hepatitis C virus, useful for modulating the expression and/or replication of hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease state in a patient. The present sequence represents an HCV hammerhead ribozyme target substrate sequence which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.38+02; ive 0; Mismatches 2; Indels
                                                                                                                                                               Hepatitis C virus hammerhead ribozyme substrate sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
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                                        AEB74336 standard; RNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                         15-PEB-2000; 2000US-00504231.
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00274553
                                                                                                                      (first entry)
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MCSWIGGEN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-215899/27
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                                                                                                                                                                                                                                                              Hepatitis C virus
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                                                                                AEB74336;
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(MCSW/)
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RESULT 198
AEB74336/c
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Macejack D;

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The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders atteming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alzheiner's disease, atherosclerosis, and restenosis. The present nucleic acid represents a human PLA2-specific monoclonal antibody heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feng X;
                                                                                                                                                   human, monoclonal antibody, phospholipase A2; PLA2; inflammatory disorder; degenerative disorder; joint inflammatory reaction; skin inflammatory reaction; blood vessels inflammatory reaction; arthritis; psoriasis; asthma; Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human phospholipase A2-specific mAb heavy chain DNA sequence #15.
                                                                                                                         Human phospholipase A2-specific mAb heavy chain DNA sequence #13
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Pred. No. 1.38+02;
0; Mismatches 2; Indels
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                             BP.
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85.7%;
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                             ADP47133 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP47135 standard; DNA; 15
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                                                                                          (first entry)
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nocerini MR;
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                                                                                                                                                                                                                                                                                                                                                                                                            (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chain DNA sequence
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                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                          09-SEP-2004
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                                                            ADP47133;
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RESULT 199
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Local Similarity 85.7 hes 12; Conservative

Matches

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02-DEC-2003; 2003WO-US038234.
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Best Local Similarity
These 12; Conserva
                                                                                                                              WPI; 2004-461119/43.
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                                                                                                                                                                                                                                                                                                                                  chain DNA sequence.
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                                                                                        Landes GM,
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                                                 (ABGE-)
                                                               (LEXI-)
                                                                                                      Jia X,
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                                                                                                                                                                                                                                                                                                                             New human monoclonal antibody that binds to phospholipase A2 (FLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                Feng X;
                      inflammatory disorder; degenerative disorder;
Johnt inflammatory reaction; skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; monoclonal antibody; phospholipase A2; PLA2;
inflammatory disorder; degenerative disorder;
joint inflammatory reaction; skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
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                                                                                                                                                                                                                                                               Liang ML,
         monoclonal antibody; phospholipase A2; PLA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               Lee YR,
                                                                                                                                                                                                                                                                                                                                                                                  Example 5; SEQ ID NO 50; 128pp; English.
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                                                                                                                                                                                                                                                               Haak-Frendscho M,
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                                                                                                                                                                                              02-DEC-2002; 2002US-0430724P.
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(LEXI-) LEXICON GENETICS
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hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain DNA sequence.
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                                                                                                                                                                                                                                                             Landes GM,
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            human;
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The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, and represent nucleic acid represents a human PLA2-specific monoclonal antibody heavy
                                                                                                                                                                                                                                                                                         New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
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joint inflammatory reaction; skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psortasis; asthma;
Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15;
                                                                                                                                                 Liang ML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; monoclonal antibody; phospholipase A2; PLA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
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85.7%; Pred. No. 1.3e+02;
                                                                                                                                              Lee YR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee YR,
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                                                                                                                                              Chen L,
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                                                                                                                                              M, Haak-Frendscho M, Nocerini MR;
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Nocerini MR;
02-DEC-2002; 2002US-0430724P.
                                                    ABGENIX INC.
LEXICON GENETICS INC
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                                                                                              The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLAZ). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma. Alzheimer's disease, atherosclerosis, and restenosis. The present nucleic acid represents a human PLAZ-specific monoclonal antibody heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a kit for detecting aquatic animal pathogens and human pathogens, comprising a pair of PCR primers used to detect specific DNA fragments of Vibrio fluvialis. The kit and method can be used in bacteria tracking and detection of aquatic animal pathogens in the course of breeding and also in the clinical detection of human intestinal acute infections, as well as in environmental monitoring. This sequence
useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kit for diagnosing gene of pathogenic bacterial and river vibrion of aquatic animal and human and testing method thereof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections, as well as in environmental monitoring. This sequence represents a PCR primer used in the scope of the invention.
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                                                                                                                                                                                                                                                                                                                         14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 Seguence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                          Example 5; SEQ ID NO 37; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2004; 2004CN-00015461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2004; 2004CN-00015461.
                                                                                                                                                                                                                                                                                                                                                                                                         GGATACAACTCTGG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB19896 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATACAGCTATGG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-296834/31.
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                              chain DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio fluvialis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  He J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1560273-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deng X,
                                                                                                                                                                                                                                                                                                                                                               Matches
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The inventors claim vectors for the expression of heterologous proteins in mammalian cells. Each vector has a first and second consensus sequence (CS). The CS or their homologues are present in Known murine autonomously replicating sequences (MuARS). The first CS is homologous to ANN92945. The inefficient selection system comprises the tk gene and a truncated tk promoter. The vectors also contain a gene coding for a protein and the necessary promoter and terminator sequences for the expression of this gene. The expression vectors provide rapid amplification, allow selection of best clones in a short time, are of universal utility in mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vectors for mammalian cells - with two consensus sequences and inefficient selection system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 324020 for detecting SNP TSC0031735
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                                                                                                                                                                                                                             Murine autonomously replicating sequence; consensus sequence; mammalian expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10.4; DB 1; Length 12; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                  Consensus sequence for mammalian expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells, and are free of viral origin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                     AAN92945 standard; DNA; 12 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 8; 12pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                87DE-03730246.
                                                                                                                                                                                                                                                                                                                                                                    88EP-00114317
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34 TCCTCTGAGAGGTA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2002 (first entry)
                         rccrcrccccaccaa 2
                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grummt F, Weidle U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1989-078357/11.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    02-SEP-1988;
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                                                                                                                                                                   01-JUL-1990
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                            15
                                                                                                                                     AAN92945;
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                                                                                                                                                                                                                                                                            Mouse.
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Gaps

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14.0%; Score 10.8; DB 1; Length 15; 85.7%; Pred. No. 1.3e+02; tive 0; Mismatches 2; Indels

Query Match
Best Local Similarity 85.7
Matches 12; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 285878 for detecting SNP TSC0012487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 13.5%; Score 10.4; DB 1; Length 12; 1 Similarity 91.7%; Pred. No. 1.2e+02; 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 324020; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                   Berlin
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                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCCAGCGAAG 1
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                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
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                                                                WO200177384-A2
                                 Homo sapiens
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                                                                                               18-OCT-2001.
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                                                                                                                                                                                                                                  Olek A,
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                         set or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 285878; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
                                 Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABI17646 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GAGAGGTAAAGA 51
                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAGGTAAAAA 1
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                                                                                                       WPI; 2001-657177/75
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                                     Olek A,
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DA AB117646

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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR0010-ABC9989, ABR0010-ABS9989, ABR0010-ABS9989, and ABI0010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastem, gastem, gasteming respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABR59989, ABR00010-ABR99989, ABR00010-ABR99989, ABR00010-ABR99989 and ABI00010-ABR82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 318752 for detecting SNP TSC0028845.
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                   13.5%; Score 10.4; DB 1; Length 12; 91.7%; Pred. No. 1.2e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                           Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABI18779 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                           41 AGAGGTAAAGAG 52
                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAAGGTAAAGAG 12
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Seguence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                      Gaps
                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 333569 for detecting SNP TSC0037605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Score 10.4; DB 1; Length 12;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 333569; 29pp + Sequence Listing; German
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                                                                                                                                                                                               ABI33596 standard; DNA; 12 BP
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 Query Match 13.5%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                        39 TGAGAGGTAAAG 50
                                                                                                1 TGAGAGATAAAG 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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AAX22517
ID AAX2251
XX
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ngs.res

Ribozyme, retinal degradation, retinal disease, learning, memory; amylotropic lateral sclerosis; tumour suppression; ss.

Aurine p16 coding sequence fragment.

32-MAR-2001 (first entry)

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This invention describes the use of novel acidophilic and thermostable xylanase enzymes (XYL I and XYL II) from Actinomadura sp. PC7 which retain their activity under harsh industrial conditions (e.g. high temperature or wide pH ranges) and may be secreted by recombinant host calls, to treat plant biomass. Xylanases XYL I and XYL II are part of a large group of hemicallulase enzymes and function by cutting the beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose residues that is a major constituent of hemicallulose). This means that they may be used in the paper and pulp industry to improve the efficiency of the heaching process by degrading the structure of the material. XYL I and XYL II may also be used to treat feed, by degrading a substrate with a high beta-glucan or callulose content. XYL I and XYL II retain their activity at high temperatures (e.g. 7) deg. C) and at low pHs (e.g. 4.0), conditions which tend to denature most known xylanases. Enzymes that remain active in these conditions may be used in industrial processes that are carried out at high temperature and low pHs to speed up other, non-enzymatic reactions, minimish costs, energy requirements, and the facilitate chlorine blacching of paper pulp which is a carried out in hot, acidic conditions). Pretreatment with XYL II and XXL II, allows the bleaching agents to penetrate better, to remove lignin from the pulp and secular can be used to produce the same or a better result. Also, disrupting the structure aids water drainage. NOTE: This patent is an equivalent to PI9503640. (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New acidophilic and thermostable xylanase enzymes from Actinomadura sp. PC7 - useful for treating plant biomass, especially paper and wood pulp, to degrade hemicellulose and hydrolyse xylan.
                                                                                                                                             Xylanase; acidophilic; thermostable; XYL I; XYL II; plant biomass; hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper; pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin; ds.
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                                                                                                       Streptomyces sp. aaaC7 gene RBS RNA fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                             94US-00282197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brzezinski R,
                                          (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-141348/14.
                                                                                                                                                                                                                                       Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1994;
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                                        25-MAR-2003
21-MAY-1999
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AAX22517;
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8XXCCCCCCCCCCCCCCCCCCCCCCX
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Novel methods for identifying genes with selected functions comprising contacting genes with a library of ribozymes, useful for identifying genes involved in, e.g. retinal disease, learning or memory and tumor

Claim 16, Fig 7, 111pp; English.

suppression.

Burger C;

Hauswirth WW, Teschendorf C,

Lewin AS, Muzyczka N, (UYFL ) UNIV FLORIDA

WPI; 2000-687548/67.

28-APR-2000; 2000WO-US011509,

WO200066780-A2

Мив вр.

09-NOV-2000

99US-0131942P

30-APR-1999;

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BP
       ABH39407 standard; DNA; 13
                          (first entry)
                                                                     WO200177384-A2
                                                             Homo sapiens
                          22-FBB-2002
                                                                              18-OCT-2001
                 ABH39407;
RESULT 212
     ABH39407,
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                                           Gaps
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AAC88504 standard; RNA; 13 BP.

RESULT 211 AAC88504 ID AAC8

Local Similarity 75.

GCGAAGCTGATG 67 GCGACGCUGAUG 13

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ö The present invention relates to a method for identifying a gene with a selected function comprising contacting genes with a library of ribozymes and identifying at least I ribozyme that alters the selected function of the gene. The present sequence is a target sequence used in the present invention. The methods (and ribozymes) are useful for identifying novel genes involved in retinal degradation, retinal disease, learning or memory, amylotropic lateral solerosis or tumour suppression, and for producing non-human animal models of diseases SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps ö Oligonucleotide SEQ ID NO 239384 for detecting SNP TSC0058391. 13.5%; Score 10.4; DB 1; Length 13; 66.7%; Pred. No. 1.3e+02; ive 3; Mismatches 1; Indels Sequence 13 BP; 1 A; 4 C; 5 G; 0 T; 3 U; 0 Other; 8; Conservative 29 TGGAGTCCTCTG 40 1 UGGAGUCCGCUG 12 Query Match Best Local Similarity Matches 8; Conserv 셤 Š

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                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABR00010-ABF99989, ABR00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPD at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
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06-APR-2001; 2001WO-IB000713.
                                        07-APR-2000; 2000DE-01019173
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                                                                                                                              Piepenbrock C,
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                                                                                 (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                methylation status.
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11D ABP72

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                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF80013 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically precreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 13.5%; Score 10.4; DB 1; Length 13; 1 Similarity 91.7%; Pred. No. 1.3e+02; 11; Conservative 0; Mismatches 1; Indels
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Claim 1; SEQ ID NO 132918; 29pp + Sequence Listing; German.
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ID ABF46225 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                               Oligonucleotide SEQ ID NO 204720 for detecting SNP TSC0050222.
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                                                            13.5%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels
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                                     Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other,
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
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ABH04743/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                           Oligonucleotide SEQ ID NO 239383 for detecting SNP TSC0058391.
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ABH39406 standard; DNA; 13
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Olek A, Piepenbrock C,
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system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 1.3e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequence
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR0010-ABH99989 and ABI0010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genemic DNA. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABH99999 ABF00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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 13.5%; Score 10.4; DB 1; Length 13; llarity 91.7%; Pred. No. 1.3e+02; Conservative 0; Mismatches 1; Indels
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Query Match
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Sequence 13 BP; 1 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                        Oligonucleotide SEQ ID NO 36765 for detecting SNP TSC0011511.
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ABC36748;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and methololic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                               Claim 1; SEQ ID NO 195649; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABF46224 standard; DNA; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AGAGGTAAAGAG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGGTAAAGTG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-657177/75.
                                                                       methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nethylation status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FBB-2002
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ABP46224

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ABP6

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The present sequence represents the preferred target sequence of an enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the Hepatitis C virus (HVC) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme cleavage sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by chucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hiterferon to treat HCV infection, other infectious diseases, autoimmune carcinoma. The ribozymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bnzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
cirrhosis; liver fallure; hepatocellular carcinoma; interferon; cancer;
autoimmune disease; ss.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel ribozymes for the treatment of diseases and conditions related hepatitis C infection.
                                                                                                                                                                                    Gaps
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                                                                                                                                             13.5%; Score 10.4; DB 1; Length 13; 91.7%; Pred. No. 1.38+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Substrate for hairpin ribozyme which cleaves HCV at nt. 886.
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                                                                                                             Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 94; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                AAZ64698 standard; RNA; 14 BP.
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98US-0100842P.
99US-00257608.
99US-00274553.
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                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2000 (first entry)
                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                     39 TGAGAGGTAAAG 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-062023/05.
                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09955847-A2
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25-FEB-1999;
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                                                                                                                                                  Query Match
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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV into the substrate sequences defined in the specification. The HCV into transpares are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more condition associated with HCV infection in conjunction with one or more condition associated with HCV infection in conjunction with one or more interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note: Some of the sequence data for this patent was brinted specification. The complete sequence data for this patent was obtained in electronic format directly from the USPFO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme; HCV expression, HCV replication, cirrhosis, virucide, liver failure, hepatococlullar carcinoma, HCV infection, drug therapy, type I interferon, interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon, hepatotropic, antiinflammatory; substrate; hairpin ribozyme; HP ribozyme; se.
                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus substrate #20 for HCV hairpin ribozyme #20.
13.5%; Score 10.4; DB 1; Length 14; 50.0%; Pred. No. 1.4e+02; ive 5; Mismatches 1; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                       ABX01535 standard; RNA; 14 BP
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                                                                              6; Conservative
                                                                                                                                                 62 CTGATGTCCTGT 73
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cuccucucucu 12
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MCSWIGGEN J A.
ROBERTS B.
PAVCO P A.
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                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
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           Query Match
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Score 10.4; DB 1; Length 14; Pred. No. 1.4e+02;

13.5%; 50.0%;

Best Local Similarity

Query Match

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The invention relates to an enzymatic nucleic acid molecule which specifically cleaves minus strand RNA derived from hepatitis C virus (HCV). The binding arms of the molecule comprise ribozyme sequences. The molecule is selected from inozyme, G-cleaver, DNAzyme, Amberzyme, and conjugate motifies. Also described: (1) a pharmaceutical composition.

Zinzyme motifis. Also described: (1) a pharmaceutical composition comprising the novel enzymatic nucleic acid; (2) a mammalian cell including the novel enzymatic nucleic acid; (3) an expression vector comprising a nucleic acid sequence encoding at least one enzymatic nucleic acid molecule, in a manner, which allows expression of that molecule; (4) a mammalian cell including an expression vector of (3); (5) methods for treating cirrhosis, liver failure or hepatocellular carcinoma by administering to a patient the novel enzymatic nucleic acid or the vector of (3); (6) a method of treating cells of the patient with the nucleic acid molecule, and further employing one or more drug the nucleic acid molecule, and further employing one or more drug the nucleic acid molecule, and further employing one or more drug cell by administering the novel enzymatic nucleic acid, and (8) a method of cleaving a separate RNA molecule by contacting the novel enzymatic collision of cleaving a separate RNA molecule. The enzymatic nucleic acid acid and the the separate RNA molecule. The enzymatic nucleic acid cid cid cid cid cid any also be used to treat or prevent the cocurrence of a disease state in a patient. The present tencer represents an HCV hairbul ribozyme target substrate sequence represents an HCV hairbul ribozyme target substrate sequence represents in the expression of the present invention.
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                                                                                                                                                                                                                                                                                                                         ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection; antiviral; gene therapy; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New enzymatic nucleic acid molecule, which specifically cleaves minus strand RNA derived from hepatitis C virus, useful for modulating the expression and/or replication of hepatitis C virus.
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  Indels
                                                                                                                                                                                                                                                                                            Hepatitis C virus hairpin ribozyme substrate sequence.
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  Mismatches
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                                                                                                                                                                         AEB76459 standard; RNA; 14
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  6; Conservative
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1 CUGCUGUCCUGU 12
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MCSWIGGEN J A.
ROBERTS E.
                                      62 CTGATGTCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
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(PAVO/)
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  Matches
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AAQ99394-Q99396 are primers used to identify DNA from both allogeneic and syngeneic sources to determine where a specific gene is expressed. The ATF-1 gene is a differentially expressed allogarift gene which is expressed allogarift gene which is expressed allogarift is an educing transplant rejection. Identification of the AIF-1 product (AAR80520) or transcript indicates that allograft rejection is taking place. The human AIF-1 gene and product are therefore useful in the diagnosis of transplant rejection. The diagnosis of transplant rejection. The diagnostic methods stage and require only a small amount of biopsy material
                                                                                          AIP-1, allograft inflammatory factor 1; transplant rejection; inhibitor; immunogenic; detection; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Differential display of mRNA; reverse transcription; DDRT-PCR; human; chondrocyte; gene specific; primer; probe; isolation; interleukin-lbeta; IL-lbeta; diagnosis; connective tissue disease; oseteoarthritis; rheumatoid arthritis; polymerase chain reaction; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding allograft rejection factors and immunogenic fragments useful for identifying transplant rejection inhibitors.
                                                         Syngeneic and allogeneic transplant comparison primer, OPA-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  Utane U;
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-240668/31.
                                                                                                                                                                                         W09517506-A1
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                   12-FEB-1996
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                                                                                                                                                                                                                            29-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                  Russell ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP705842-A2
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                                                                                                                                                     Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two primers are used to amplify any given mRNA molecule in its CDNA form. The first primer is capable of binding either to (1) a site immediately upstream of the first adenine nucleotide of the poly A tail; (2) to a site including the mRNA's poly A signal sequence; (3) to a site including the mRNA's poly A sequence of an mRNA of which the nucleotide sequence or (4) to a sequence of an mRNA of which the nucleotide sequence is known. These primers are then extended by reverse transcriptase to produce the corresponding cDNA sequence. The second primer comprises an arbitrary sequence and is used alongside the first primer to amplify the cDNA molecule by PCR. This primer is a second arbitrary primer. (Updated on 25-MAR-2003 to correct PN field.)
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    mRNA; primer; PCR; polymerase chain reaction; poly A site; RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning and isolating mRNA as cDNA - by reverse transcription and polymerase amplification using two oligo-deoxy-nucleotide(s).
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             Score 10.4; DB 1; Length 14;
Pred. No. 1.4e+02;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                         reverse transcriptase; kozak sequence; вв.
                                                                                                                                                                                                                                                                                                                                                                Primer for production of cDNA from mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kxample 4; Page 17; 43pp; English.
                                                                                                                                                                                                                                BP.
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93US-00033084.
               13.5%;
50.0%;
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(first entry)
Query Match
Best Local Similarity 50.0-
                                                                                          62 CTGATGTCCTGT 73
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cuecueuccueu 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liang P, Pardee AB;
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11-MAR-1993;
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23-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                   AAQ47917;
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AAQ479177
AAQ47917
AAQ479

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AAQ99394 ID AAQ9 XX AC AAQ9

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                                                                                                                                                                                     The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which were used along with 4 degenerate 3' oligo dT primers for the differential display of human chondrocyte mRNA by reverse transcription and FCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA clones, which were then searched against DNA databases for homology to known human genes. The cDNA mols. can be used for the prodn. of gene specific primers and probes to isolate genes induced by treating (esp. human) chondrocytes with interleukin-lbeta (IL-lbeta), and for the diagnosis of IL-lbeta related connective tissue diseases, in partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia - and/or predisposition to develop premature atherosclerosis by detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dhc-1; homocysteine; hypohomocysteinaemia; atherosclerosis; diagnosis; serum; Dami cell; PCR; arbitrary primer; messenger RNA pool; ss.
                                                                                                           osis and treatment of IL-1 mediated connective tissue diseases - osteopontin, calnexin, TSG-6 gene prod., genes encoding them or
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                      13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RES DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increased levels of serum homocysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 22; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HAMI-) HAMILTON CIVIC HOSPITALS
                                                                                                                                                               Example; Page 15; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weitz J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT75144 standard; DNA; 10 BP
94EP-00115751
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arbitrary RT-PCR primer.
                                                                                                            Diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCCAGCGAA 10
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                                                      Margerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-372877/34.
                                                                                 WPI; 1996-181045/19.
                                                                                                                         using osteopontin, antibodies to them.
                           (FARH ) HOECHST AG.
06-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-1998
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                                                      Bartnik E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT75144;
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                discrete fractions which were increased or decreased were identified.

This method was used to identify mRNA and the corresponding cDNA which are increased in the cells of a patient having hyperhomocysteinaemia or a predisposition to homocysteine mediated atherosclerosis. These polynucleotides can be used for the diagnosis and treatment of atherosclerotic diseases and diseases of metabolism of sulphur containing amino acids (e.g. homocysteinaemia), which are associated with vascular damage and atherosclerotic disease, specifically unstable angina, acute myocardial infarction (heart attack), cerebrovascular accidents (stroke), hypertension, renal artery stenosis, aortic stenosis and deep vein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primers AAV10683-V10688 are used to obtain novel human breast cancer genes by differential display. The identified genes or fragments of these genes can be used for identifying genes and gene products that are intimately related to malignant transformation or maintenance of the malignant properties of cancer cells. It can also be used to design or screen diagnostic reagents or therapeutic compounds. Kits are included within the scope of the invention
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Breast cancer genes - used to develop products to design or screen diagnostic reagents or therapeutic compounds.
homocysteine. PCR products were separated on a sequencing gel and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breast cancer; malignant transformation; diagnostic; therapeutic;
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                                                                                                                                                                                                                                                                                                13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast cancer gene differential display primer #6.
                                                                                                                                                                                                                                                           Seguence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV10688 standard; DNA; 10 BP.
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96WO-US009286.
96US-0019202P.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-512705/47.
                                                                                                                                                                                                                                                                                                                                                                                51 AGCCAGCGAA
                                                                                                                                                                                                                        occlusive disease
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05-JUN-1996;
06-JUN-1996;
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                                                                                                                                                                                                                                                                                                    Query Match
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RESULT 234

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New Brassica napus nucleic acid and protein, useful for regulating pod dehiscence and/or plant abscission by producing transgenic plants or propagating material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer AAX34944-45 were used to amplify DNA encoding a dehiscence zone protein designated ORS7(9). The ORS7(9) polymucleotides and polypoptides are useful for regulating pod dehiscence and plant abscission. Antisense ORS7(9) nucleic acid useful for preventing or reducing dehiscence or abscission.
                                                                                              PCR primer for DNA encoding a dehiscence zone protein ORS7(9).
                                                                                                                                Dehiscence zone protein; ORS7(9); regulation; pod dehiscence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal transduction protein; dehiscence; male sterile plant;
shatter resistance; oilseed rape; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.18+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                     plant abscission; PCR primer; ss
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                                                          28-JUN-1999 (first entry)
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Matches 10, Conservative
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                                                                                                                                                                                                        Brassica napus.
                                                                                                                                                                                                                                                                                                                  18-SEP-1998;
                                                                                                                                                                                                                                          WO9915680-A1
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                                                                                                                                                                                       Synthetic.
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                          AAX34945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primers AAV15590 and AAV15591 are used to amplify fragments of the C4.8 and C21.7 genes from a human papillomavirus (HPV) immortalised human foreskin keratinocyte cell line HFR-1A. These genes are characteristic of late or early passage cells can be used in a method for assessing the potential for progression of cervical lesions. Antibodies generated and to assess potential for lesion progression. Antibodies can also be used therapeutically by inhibiting the polypeptide are used to an also be based on the nucleotide sequence are used to inhibit expression of the protein. Detecting polypeptides, or related RNA, characteristic of late passage cells (which are potentially malignant) in cervical smears is a reliable way of assessing progression potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid characteristic of late or early passage cells immortalised by papilloma virus - and related polypeptide(s) and antibodies, used for diagnosis and treatment of cervical cancer and assessing potential for progression of cervical lesions.
                          Gaps
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                                                                                                                                                                                                                                                                                                                            Cervical cancer; treatment; diagnosis; passage cell; lesion; human foreskin keratinocyte cell line; HPK-1A; antibody; smear;
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   100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indele
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                                                                                                                                                                                                                                                                                            Human HPK-1A C4.8 and C21.7 PCR primer AP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                                                                                                                                  AAV15590 standard; DNA; 10 BP.
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  PCR primer; 88.
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AAV15590

AAV15590

AAV2

AAV3

Best Loca Matches

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AAX34945 ID AAX3

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(BIOG-) BIOGEMMA UK LTD

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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a primer used to amplify Rin2 cDNA sequences. Rin2 polypeptides downregulate functional responses elicited by Ras-dependent signalling pathways. Agents that increase Rin2 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rin2; downregulation; functional response; allergy; asthma; hayfever; Ras-dependent signalling pathway; allergy; asthma; hayfever; atopic cozema; Ras-dependent cance; neoplastic cellular proliferation; autoimmune disease; T cell-associated disease; T cell dependent graft vs. host disease; type I diabetes mellitus; multiple sclerosis; Crohn's disease; autoimmune hepatitis; psoriasis; wound healing; angiogenesis; re-epithelialization; numnune deficiency virus; immune suppression; cancer therapy; nerve regeneration; PCR primer; ss.
                                                                                              A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants.
                                                                                                                                                                                                                                                                                                                                  13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer AP-1 used to amplify Rin2 cDNA sequences.
                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
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                               Whitelaw C;
                                                                                                                                                Example 1; Page 23; 71pp; English.
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97US-00942819
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Matches 10; Conservative
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                               Roberts JA,
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                                                              WPI; 1999-580449/49
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02-OCT-1997;
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                               Wyatt P,
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The present invention describes nucleic acids comprising human, murine or rat cDNAs encoding DRM proteins (derived from the down-regulated in v-mos transformed calls, drm gene). The nucleic acids, and DRM proteins, are useful for arresting call growth; inhibiting tumour call growth; treating hyperproliferative cellular disorders, either in vivo or ex vivo and producing fusion proteins with enhanced green fluorescent protein (BGFP) of increased stability (useful in screening assays, protein-protein interaction studies, cell labeling and as markers during purification). Detecting abnormally low levels of DRM, or the nucleic acids, may be used to identify subjects with an increased risk of developing as useful as probes and primers to detect or quantify drm and to screen genomic and convex introduces raised against DRM can be used to convex in immunoassays. Pusion proteins of DRM and GFP are localised to the nucleus (in contrast cytoplasmic localisation of GFP ö (particularly Rin2 itself, optionally expressed from a vector) are used to treat allergy (asthma, hayfever or atopic eczema); Ras-dependent cancers and (non-)neoplastic callular proliferation; autofmumue diseases; T cell-associated diseases and T cell dependent graft vs. host disease (typical examples being type I diabetes mellitus; multiple sclerosis, Crohn's disease, autoimmune hepatitis and psoriasis). Agents that inhibit Rin2 activity are used to improve wound healing; angiogenesis and/or respithelialization (also to improve immune response to pathogens; in human immune deficiency virus, and some other, infections; immune suppression associated with cancer therapy, and nerve regeneration) DRM; secreted protein; cell growth inhibition; fusion protein; tumour; green fluorescent protein; GFP; hyperproliferative cell disorder; enhanced green fluorescent protein; BGFP; diagnosis; PCR primer; ss. New isolated nucleic acid encoding DRM protein, for regulation of cell growth, particularly treating cancer and. Gaps ö 13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels Calothy G; Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other; Marx M, (USSH ) US DEPT HEALTH & HUMAN SERVICES. Example 1; Page 31; 115pp; English Topol LZ, 뗦. 99WO-US006675 98US-0079440P AAZ25357 standard; DNA; 10 17-DEC-1999 (first entry) Query Match
Best Local Similarity 100.
Matches 10, Conservative Blair DG, Clausen PA, 9 1 AGCCAGCGAA 10 Rat DRM PCR primer #1. WPI; 1999-591095/50. 51 AGCCAGCGAA WO9949041-A1 26-MAR-1999; 26-MAR-1998; 30-SEP-1999 Rattus sp. Synthetic. AAZ25357; RESULT 238 8888888888888 셤 ଚ

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RESULT 240
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itself) and so are more stable, e.g. on exposure to fixatives or detergents, and thus form more versatile reagents, e.g. they can be used in fluorescence-based assays that require cell fixation, or linked to proteins or antibodies for use in enzyme-linked immunosorbent assays. Stable EGFP can be attached to proteins during synthesis, allowing the labeling of materials that are too unstable for chemical modification. The present sequence represents a PCR primer for rat DRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cancer associated gene; cancer specific gene; C1-9a11-2; CH8-2a13-1; CH13-2a12-1; CH14-2a16-1; cancer; gene duplication; RNA overabundance; breast cancer; lung cancer; glioblastoma; pancreatic cancer; colon cancer; prostate cancer; hepatoma; myeloma; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer associated polypeptides, genes encoding them and antibodies inst them, useful for diagnosing breast cancer and screening for
                                                                                                                                                                                                                                                                                     0; Gaps
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Pred. No. 1.1e+02;
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100.0%; Pred. No. ...
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Matches 10; Conservative
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                         Query Match 13.0%; Score 10; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 10; Conservative 0; Mismatches 0; Indels
Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
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98US-0089814P.
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expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while confer transcripts correspond to novel genes. Antigen-presenting cell cher transcripts correspond to novel genes. Antigen-presenting cell (APC) -associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells, immunostimulatory cofactors also being required for cells. Tumour antigen presentation via the WHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone the tumour cells, immunostimulatory cofactors also being required for cefficient activation of cytotoxic T-lymphocytes (CTIS). Nucleic cail sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of diseases related to abnormal expression of these genes. Detection of diseases related to abnormal expression of these genes. Detection of diseases related to abnormal expression of these genes. Detection of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in active immunotherapy (or to stimulate production of the mannary adequate antigen presentation of co-stimulatory factors enumers adequate antigen presentation of co-stimulatory signals, migration of chemokines and
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SA-inducible gene; transgenic plant; pathogen resistance; FCR primer; ss.
Isolated polynucleotides differentially expressed in antigen-presenting
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                                                                                                                 SAGE (serial analysis of gene
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                       cells, useful in gene vaccines against cancer.
                                                                                                            Sequences AAZ77573-Z79709 represent
                                                                    Claim 1; Page 125; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ50856 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0095187P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ACAAGACGGC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200008186-A1
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                                                                                                                                                                       The patent discloses fifteen new salicylic acid (SA) inducible genes from Nicotiana tabacum, nine of which were subcloned and sequenced. Based on Aifferent Kinetics of induction response, these genes were classified into four categories, class I, II, III and IV response genes. The SA-inducible genes are useful for making transgenic plants with enhanced pathogen resistance. The plants incorporating these genes show reduced susceptibility to fungal pathogens. The present sequence is an upstream primer API used in differential display PCR reactions along with downstream primers T12MG or T12MC to identify tobacco SA-inducible genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of microorganisms and viruses, for use in the food and cosmetic industries and for clinical diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a novel in vitro method for the detection of microorganisms and viruses. The method comprises: (1) forming a polymerase chain reaction (PCR) mixture by combining a predetermined volume of a sample to be tested for the presence of a nucleic acid sequence comprising 5. TAGAAGC-3', known amounts of a first primer comprising 5. GCTAAGGTCCCAAAGG-3', and a second primer comprising 5. GCTAAGGTCCCAAAGG-3', and product by AGAAGCCTCCTACC-3', and PCR reagents; (2) forming a PCR product by
                                                                                    Novel salicylic acid inducible genes from tobacco plants, useful for making transgenic plants with enhanced pathogenic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microorganism; virus; polymerase chain reaction; food; cosmetic; clinical diagnostic; molecular beacon; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                  Chua N;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                  Horvath DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 25; 63pp; English.
                                                                                                                                           Example 1; Page 51; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ48447 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer specific for C. jejuni.
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es 10; Conservative
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                  Jepson I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 AGCCAGCGAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-086985/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campylobacter jejuni
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17-MAY-1999;
                  Stuiver MH,
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Matches
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100.08;

Best Local Similarity

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cycling the PCR mixture to amplify the nucleic acid sequence, if present, to replicate and attain 0.25-10000mug nucleotide product/mul mixture; (3) adding a probe containing DNA comprising S'-GGTGGCTCTTAAGCCACC-3' to the PCR mixture or to the PCR product to cause the DNA to hybridize with the nucleic acid sequence, if present, and change the conformation of the probe; and (4) determining whether or not bacteria are present in the sample by detecting the conformational change indicating the presence of bacteria in the sample. The methods can be used for the detection of viruses and microorganisms, including bacteria, yeast, molds and protista. They can be used in the food and cosmetic industry and in clinical diagnostics. Using the method it is not necessary to remove non-hybridized probe from the system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes isolated DNA (I) encoding an allograft inflammatory factor-1 (AIF-1). AIF-1 has immunosuppressive, antiinflammatory and antiarteriosclerotic activities. AIF-1 is an inhibitor of expression of allograft factor such as Gal/GaINAc macrophage lectin. AIF-1 is useful for diagnosing and treating allograft rejection and other conditions associated to vascular inflammation, especially atherosclerosis. The present sequence represents a PCR primer which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allograft inflammatory factor 1; AIF-1; AIF-2; allograft gene; screening diagnosis; allograft rejection; vascular inflammation; atherosclerosis; immunosuppressive; antiinflammatory; antiarteriosclerotic; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding an allograft inflammatory factor-1, useful for diagnosing and treating allograft rejection and other conditions associated with vascular inflammation, especially atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA65614 standard; DNA; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AGCCAGCGAA
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Best Local Similarity
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AAA651.
AAA6551.
AAA6
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13.0%; Score 10; DB 1; Length 10;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
                                                                                                                                                                                                                                            Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
              Gaps
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                                                                                                                                                                                                                    Human kidney specific transcriptome sequence SEQ ID NO: 222
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              Indels
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Pred. No. 1.1e+02; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2000; 2000WO-US031922.
                                                                                                                                      AAH63382 standard; cDNA; 10
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                                                                                                                                                                                           (first entry)
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              Conservative
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                                                                 1 AGCCAGCGAA
                                         51 AGCCAGCGAA
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                                                                                                                                                                                                                                                                                        Homo sapiens
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              10;
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                                                                                                           RESULT 244
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              Matches
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AAF37199 standard; DNA; 10
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              WO200077214-A2
                          16-JUN-1999;
                  21-DEC-2000
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                                                                                                                                         RESULT 246
                                                                                                                          Matches
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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   method, in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Velculescu V, Vogelstein B, Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 152; 419pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00335032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNIX40H SNHOL VINU ( OLYU)
                                                                                                                                                                                                     Saccharomyces cerevisiae
                                                                                                                             linker; PCR primer; ds.
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The present lime present lime present coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes coding sequence of a yeast gene septession) tag. Also described are: (1) a method (M1) of using NORF gene expression) tag. Also described are: (1) a method (M1) of using NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate by at candidate antifungal drug comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression congrising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORP gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell with a candidate drug as a member of a yeast cell comprising contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and contacting a yeast cell of at least 1 NORP genes may be used to identification of the cell of the cell cycle, the differentially cycle and for identification of antifungal drugs. APF33268 to AAF44064.

AAF33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention. The present invention describes an isolated DNA molecule comprising a

ö Gaps ö 13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; 0; Indels 100.0%; Pred. No. Local Similarity 100. 47 AAAGAGCCAG 56 10 AAAGAGCCAG 1

RESULT 247 AAF36709/ ID AAF3 XX BP

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3938.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2. 

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

(UYJO ) UNIV JOHNS HOPKINS.

99US-00335032

16-JUN-1999;

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 140; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonamotated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate or antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human genes which are involved in cell cycle progression of identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and conting expression in the yeast cell of at least 1 NORF gene whose expression in a yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene whose expression in the yeast cell of at least 1 cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064.

AAF33262 to AAF33267 trepresent linkers and PCR primers used in the seamplation of the present inventor. method, in the exemplification of the present invention

Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Gaps ö Score 10; DB 1; Length 10; Pred. No. 1.1e+02; 0; Indels 0; Mismatches 100.08; 13.0%; Query Match
Best Local Similarity 100.

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27 18 GGATACAACT 10 GGATACAACT

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AAF36709 standard; DNA; 10 BP.

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nor previously assigned open reading frame; nonamnotated ORF; SAGB; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                       Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3448
                                   Yeast; Saccharomyces cerevisiae; characterisation; cell
                                                                                                                                        Kinzler K;
                                                                                                     14-JUN-2000; 2000WO-US016223.
                                                                                                                99US-00335032
                                                                                                                                        Jelculescu V, Vogelstein B,
                                                                                                                            SNING OUND (OLYD)
            23-MAR-2001 (first entry)
                                                                 Saccharomyces cerevisiae.
                                                                             WO200077214-A2.
                                                                                                                16-JUN-1999;
                                                                                         21-DEC-2000
AAF36709;
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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. WPI; 2001-061874/07.

Example; Page 123; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising a SAGE (serial analysis of gene expression) tag. Also certification and the call of the comprising a SAGE (serial analysis of gene whose expression varies by at least 10% between any two phases of the call office is selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast call; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell with a candidate drug and contacting a yeast cell with a candidate drug and cyeast cell comprising contacting a yeast cell with a candidate drug and contacting a peast of by a least of by sense whose expression in the yeast cell of at least 1 NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. App33268 to AAP44064 crepresent SAGE tages used in the exemplification of the present invention.

CARAFIRES TO AAP33267 represent 1 inkers and PCR primers used in the SAGE AAF33262 to AAF33267 represent linkers and PCR primers method, in the exemplification of the present invention

Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Gaps ö 13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; 0; Indels 100.0%; Pred. No. 1.1. 10; Conservative Best Local Similarity Query Match Matches

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AAF38884 standard; DNA; 10 BP

AAF38884;

23-MAR-2001 (first entry)

cycle; NORF;

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5623.

Yeast; Saccharomyces cerevisiae; characterisation; call cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000

14-JUN-2000; 2000WO-US016223.

16-JUN-1999;

(UYJO ) UNIV JOHNS HOPKINS.

Kinzler K, Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 200; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORP (not previoually assigned open reading frame; or nonanotated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORP genes to affect the cell comprising administering a NORP gene whose expression varies by at comprising a comprising a NORP gene whose expression or arithmial drugs comprising (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORP gene whose expression of antifungal drugs (a) contacting a test substance which modifies the expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at lm M1, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contiguous nucleotides of a NORP gene whose expression is affected by the class of the cell cycle progression in a continuous nucleotides are an administration of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle and cycle and for identification of antifungal drugs, APAF33268 to AAF431664 crepresent SAGS tags used in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE comethod, in the exemplification of the present invention. AAP3884
AAC3 AAC3
AAC3 AAC

Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

ö 13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels 10; Conservative Query Match Best Local Similarity Matches

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Gaps

셤 8

RESULT 248

ngs.res

28-JUN-2002 (first entry)

AAL42350;

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The sequence represents the rat arbitrary PCR primer AP-1, used in the invention to amplify CDNA from rat ovary tissue. The invention relates to a novel isolated UO-44 nucleic acid molecule comprising a sequence of a novelcides corresponding to a uterine cestrogen agonist-inducible corresponding to a uterine cestrogen agonist-inducible corresponding to a uterine cestrogen agonist-inducible corresponding to a meanmal. The UO-44 sequences of the invention have cytostatic activity. The UO-44 polynucleotide is useful in the candicament for the treatment of a condition in a mammal, corresponding diagnosing, detecting or monitoring uterine cancers and/or covarian cancers, and for producing the polypeptide. The polynucleotide or polypeptide is useful for monitoring uterine and ovarian growth and development and the level of cestrogenic activity in tissue including cancer tissue. They are also useful for the generation of a range of therapeutic molecules capable of modulating oestrogen agonist-mediating coll growth and proliferation in the uterus including ovaries. The UO-44 itself
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosing uterine and/or ovarian cancers, comprises sequence corresponding to uterine estrogen agonist-inducible genetic sequence in
                                                                                                                                                                                               Rat; oestrogen agonist-inducible; hUO-44; cytostatic; ovary; uterine cancer; ovarian cancer; uterine growth; uterine; development; ovarian growth; ovarian development; oestrogenic activity; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated UO-44 nucleic acid molecule useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NACA-) NAT CANCER CENT SINGAPORE PTE LTD. (HUGH/) HUGHES E J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 37; 82pp; English
                                                                                                                                                            Rat arbitrary PCR primer AP-1.
                                       AAH77187 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2001; 2001WO-AU000379.
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15-AUG-2000; 2000AU-00009471.
                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                    Rattus norvegicus
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                                                                                                                     24-JAN-2002
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Best Local Si
Matches 10;
                                                                              AAH77187;
                                                                                                                                                                                                                                                                 AP-1; 88.
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RESULT 249
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A new microsatellite DNA derived from a Pyrus plant and discrimination of
                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a novel microsatellite DNA sequence derived from Pyrus plants. The invention also comprises a method for discriminating Pyrus plants - utilising the novel Pyrus microsatellite DNA. The novel microsatellite DNA sequence can be used in discriminating Pyrus plants. The present DNA sequence represents a PCR primer specific for a novel Pyrus pyrifolia (sand pear) microsatellite DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endometrium, placenta, serine protease, gynecological, cytostatic,
cardiant, PRSP, infertility, endometriosis, cancer, pregnancy, primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                          primer; novel microsatellite DNA sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                               Novel sand pear microsatellite DNA PCR primer 14.
                                                                                                                                                                                                                                                                   (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PRIN-) PRINCE HENRY'S INST MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer used during DDPCR analysis #20.
                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 5; 22pp; Japanese.
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                                                                                                                                                                                                                21-JUL-2000; 2000JP-00220339.
                                                                                                                                                                                                                                          21-JUL-2000; 2000JP-00220339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-2002; 2002WO-AU001010
                                                                                        Sand pear; ss; PCR; primer;
Pyrus plant discrimination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACF12803 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                    Pyrus plants by using it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGCCAGCGAA 10
                                                                                                                                                                                                                                                                                             WPI; 2002-298819/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AGCCAGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                Pyrus pyrifolia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003011905-A1
                                                                                                                                                           JP2002034597-A.
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                                                                                                                                                                                     05-FBB-2002
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Gaps

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Local Similarity 100 tes 10; Conservative 51 AGCCAGCGAA 60 AGCCAGCGAA 10

8

AAL42350 standard; DNA; 10 BP.

RESULT 250 AAL42350 ID AAL423

and

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The present sequence relates to a new isolated nucleic acid molecule, which is expressed in endometrium and placenta and is upregulated in pregnant uterus and is highly expressed during placental development, encodes a protein having serine protease activity and has an insulin-like growth factor (IGF)-binding motif. The compound is considered growth factor association and cardiant. The enzyme is specifically expressed in association with embryo implantation and placentation in a pregnant uterus. The nucleic acid is useful for preparing a composition for treating PRSP-related condition e.g., infertility, endometriosis, cancer or a disease of the heart, testis or ovaries. Further, it is useful for detecting, diagnosing or monitoring a condition involving a change in PRSP expression. The sequence is present in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human fructose-bisphosphate aldolase B (ALDOB) and single nucleotide polymorphisms (SNPs) which have been identified in each sequence. The method of haplotyping the sequences is useful for haplotyping the fructose-biphosphate aldose B (ALDOB) gene of an individual or for validating the ALDOB protein as a candidate target for treating a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                New nucleic acid encoding a protein having serine protease activity an insulin-like growth factor-binding motif, useful for preparing a composition for treating a pregnancy-related serum protease-related condition e.g., infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 10; DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
 Findlay JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ALDOB gene allele-specific primer SEQ ID NO: 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ALDOB; fructose-bisphosphate aldolase B; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single nucleotide polymorphism; primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. active 0; Mismatches
 Hampton AL,
                                                                                                                                                         Example 1; Page 55; 156pp; English.
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Υ,
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 Salamonsen LA,
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                                  WPI; 2003-268108/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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ACF57644/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a method of screening for candidate agents capable of altering the biological activity of a protein encoded by a nucleotide involved in hypoxia-related tumourigenesis. The method of the invention involves: contacting a test agent with a target cell expressing the nucleotide, and monitoring the activity of the expressed protein product; if the test agent modifies the activity of the expressed protein then this is a candidate agent. The method of the invention is useful for modifying hypoxia-induced gene regulation and for diagnosing, prognosing or treating tumours. The present DNA sequence represents a SAGE tag that was used in the exemplification of the invention.
condition predicted to be associated with ALDOB activity. The present sequence is an allele-specific primer/probe used to identify the haplotype of the human ALDOB gene in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying agents that alter biological activity of a polypeptide encoded by a polynucleotide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity
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                                                                                                                                     Gaps
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                                                                                       DB 1; Le...
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                                                                                                                                                                                                                                                                                                                                                                                      Hypoxia-related tumourigenesis-related SAGE tag #1470.
                                                                                                                                                                                                                                                                                                                                                                                                                   screening; hypoxia-related tumourigenesis;
hypoxia-induced gene regulation; tumour; SAGE tag; ds
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                                                                  Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
                                                                                                                                     0; Mismatches
                                                                                                     13.0%; Score 10; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                       ADU19679 standard; DNA; 10 BP.
                                                                                                                   Local Similarity 100.0%;
Les 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-2003; 2003US-0461712P.
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                                                                                       13-JAN-2005
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                                                                                                                                                                                                     10
                                                                                                        Query Match
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Matches
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Matches
                                                                                                                                                                                                                                                       RESULT 253
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WO2004092198-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 256
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a method of screening for candidate agents capable of altering the biological activity of a protein encoded by a nucleotide involved in hypoxia-related tumourigenesis. The method of the invention involves: contacting a test agent with a target cell expressing the nucleotide, and monitoring the activity of the expressed protein product; if the test agent modifies the activity of the expressed protein then this is a candidate agent. The method of the invention is useful for modifying hypoxia-induced gene regulation and for diagnosing, prognosing or treating tumours. The present DNA sequence represents a SAGE tag that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                             Identifying agents that alter biological activity of a polypeptide encoded by a polynucleotide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity
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                                                                                                                screening; hypoxia-related tumourigenesis;
hypoxia-induced gene regulation; tumour; SAGE tag; ds
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hypoxia-induced gene regulation; tumour; SAGE tag; ds
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                                                                                           Hypoxia-related tumourigenesis-related SAGE tag #237.
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                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 61, 100pp, English
                       ADU18446 standard; DNA; 10 BP
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                                                                   (first entry
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Best Local Similarity
                                                                                                                                                                            WO2004092198-A2
                                                                                                                                                     Unidentified
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                                                                                                                                                                                                    28-OCT-2004.
                                             ADU18446;
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            ADU18446/
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The invention comprises a method of screening for candidate agents capable of altering the biological activity of a protein encoded by a nucleotide involved in hypoxia-related tumourigenesis. The method of the invention involves: contacting a test agent with a target cell expressing the nucleotide, and monitoring the activity of the expressed protein product; if the test agent modifies the activity of the expressed protein then this is a candidate agent. The method of the invention is useful for modifying hypoxia-induced gene regulation and for diagnosing, prognosing or treating tumours. The present DNA sequence represents a SAGE tag that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                encoded by a polynucleotide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity
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1.1e+02;
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hypoxia-induced gene regulation; tumour; SAGE tag; ds.
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                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 97; 100pp; English.
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09-APR-2004; 2004WO-US011087.
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                                           09-APR-2003; 2003US-0461712P
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                                                                                       (GENZ ) GENZYME CORP
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encoded by a polynucleotide involved in hypoxia-related tumorigenesis comprises contacting an agent with a target cell and monitoring activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor VII mutant nucleic acid gene analysis probe, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analysis; SNP detection; factor VII; probe; ss.
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                                                                                                                                         Disclosure, Page 56, 100pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEC05483 standard; DNA; 11 BP
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                                                                        expressed product
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                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
Bpstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
                                           13.0%; Score 10; DB 1; Length 11; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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               Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                  Herpesvirus inhibiting antisense oligonucleotide.
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                                                                                                                                                                                                                                AAQ24028 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                 (first entry)
                                    Query Match
Best Local Similarity 100.
                                                                                                               33 GTCCTCTGAG 42
                                                                                                                                  GTCCTCTGAG 11
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                                                                                                                                                                                                                                                                                                   (revised)
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21-SEP-1992
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 367500 for detecting SNP TSC0056379.
                                                                                                                                                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 341012; 29pp + Sequence Listing; German.
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                                                                                                                                                                                        06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                                   07-APR-2000; 2000DE-01019173.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 277988 for detecting SNP TSC0005414.
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                                                                   ABH77995 standard; DNA; 12 BP
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                                                                                                                ABH77995;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABR0010-ABF9989, ABR0010-ABF9989, ABR0010-ABF9989, ABR0010-ABF9989, and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                         Length 12;
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                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                               Piepenbrock C,
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This invention describes novel oligonucleotide primars or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

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                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 353119 for detecting SNP TSC0010241.
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13.0%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
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            Local Similarity 100
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                        Oligonucleotide primer SEQ ID NO 281019 for detecting SNP TSC0009317.
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Les 10; Conservative
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22-FEB-2002
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ABH91914/c
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ATACAACTCT

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ABH81026 standard; DNA; 12 BP

RESULT 265
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 278381 for detecting SNP TSC0005966.
                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 291907; 29pp + Sequence Listing; German.
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                                                                                                             (RPIG-) EPIGENOMICS AG.
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                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (GNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                               Claim 1; SEQ ID NO 278381; 29pp + Sequence Listing; German
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                       13.0%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                              43 AGGTAAAGAG 52
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AB122756/C
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AB122756/C
AB12076/C
AB1276/C
AB12076/C
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 366693 for detecting SNP TSC0055920.
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                                                                                                                                                                       BP.
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Matches 10; Conservative
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11 ATACAACTCT
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13.0%; Score 10; DB 1; Length 12; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels

Local Similarity 100.

Matches

Query Match

20 ATACAACTCT 29

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF0010-ABE99989, ABT0010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT0010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99899, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE99989, ABT00010-ABE999899, ABT00010-ABE99989, ABE99989, ABT00010-ABE99989, ABT00010-ABE999
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                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format from WIPO at
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                               (RPIG-) RPIGENOMICS AG.
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Claim 1; SEQ ID NO 4039; 29pp + Sequence Listing; German.

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acid (PNA) oligomers for detecting single mucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABF00010-ABF99999 ABF00010-ABF99999 and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published\_pct\_sequences This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published\_pct\_sequences This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. ö Oligonucleotide SEQ ID NO 137935 for detecting SNP TSC0034489. Claim 1; SEQ ID NO 137935; 29pp + Sequence Listing; German. 13.0%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.5e+02; 0; Indels Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other; 0; Mismatches Berlin K; BP 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. ABF37938 standard; DNA; 13 (first entry) Query Match Best Local Similarity 100. Matches 10; Conservative Olek A, Piepenbrock C, GAGGTAAAGA 51 GAGGTAAAGA 11 (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2 Homo sapiens 21-FEB-2002 18-OCT-2001. ABF37938; 42 RESULT 274 X88688888888888888888888 셤

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                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                         Oligonucleotide SEQ ID NO 62675 for detecting SNP TSC0016605.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cyrosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azidovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nuclecide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNN. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE99899, ABC0010-ABE99899, ABC0010-ABE99989, ABC0010-ABE99989 and ABI00010-ABE8073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPD at the printed specification, but ftp.wipo.int/pub/published\_pct\_sequences SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine ö Oligonucleotide SEQ ID NO 265570 for detecting SNP TSC0064365. Claim 1; SEQ ID NO 182001; 29pp + Sequence Listing; German 13.0%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels Sequence 13 BP; 6 A; 1 C; 4 G; 2 T; 0 U; 0 Other; Berlin K; BP 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. ABH65593 standard; DNA; 13 (first entry) 10; Conservative Olek A, Piepenbrock C, 40 CACACCIAAA 49 3 GAGAGGTAAA 12 (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WPI; 2001-657177/75 methylation status. Local Similarity

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABH00010-ABH99989 and ABI00010-ABR2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABR99989, ABR00010-ABR99989, ABR00010-ABR99989, ABR00010-ABR99989, ABR00010-ABR99989, adata for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequence
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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                                                                                                                                                     Oligonucleotide SEQ ID NO 224066 for detecting SNP TSC0054592.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABE99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Oligonucleotide SEQ ID NO 4040 for detecting SNP TSC0001514
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                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at ftp.wipo.int/pub/published_pct_sequence
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                                     Claim 1; SEQ ID NO 224065; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ABH65592 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                 Oligonucleotide SEQ ID NO 182002 for detecting SNP TSC0044987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 182002; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.0%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yin yang-1 potential splice variant acceptor site #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 13 BP; 2 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
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ABF82005 standard; DNA; 13 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2001; 2001WO-IB000713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-APR-2000; 2000DE-01019173
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                                                                                                                                   22-FBB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-2004 (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) RPIGENOMICS AG
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AAV99057;
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AAV99057/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a protein variant of the Yin Yang-1 transcription factor [1], having a 411 amino acid (aa) sequence (4) reproduced. Also described are: protein (Ia) that is a homologue of (4) and includes Arg a position 303 and 11; peptide (II) that is a fragment of (II) that is a fragment of (II) that is a reagment of (II) that encodes (II), [1a) or (II); peptide (II) that is a fragment of (II) that encodes (II), [1a) or (II); an antibody (Ab) directed against (II) or (Ia); methods for determining a tendency to develop type I diabetes; transgenic non-human mammal (A) in which the germ and somatic cells contain a nucleic acid (or segment) encoding 411 as sequence (2), or sequences with at least 95, hest 99* homology, where the homologue includes 303Met and 311Arg; and use of (A) to screen for compounds (B) that are protective against diabetes. The methods are useful for modulating activity of the YY1 (YIN Yang-I) multifunctional transcription factor. (I), or its homologues and peptides, also nucleic acids encoding them and antisense oligonucleotides, are useful for treatment of type I and 2 diabetes, autoimmune diseases, cancer and disorders of mineral and lipid metabolism. Detecting mutations in the human analogue of (4) is used to determine a predisposition for these diseases. Transgenic and the protein and animals of the contain the contain and animals of the contain and animals and anima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that contain the sequence encoding (4), or its homologues, are used to screen for agents protective against diabetes. This sequence represents a potential splice acceptor site for splice variants of yin yang-1
                                                                                                                                                                                                                                                                                                                                                                          New variant of the Yin Yang-1 transcription factor, useful for treating e.g. diabetes and autoimmune disease, also for diagnosing predisposition and in screening for therapeutic agents.
transcription factor; type 1 diabetes; transgenic; diabetes;
multifunctional transcription factor; type 2 diabetes;
autoimmune disease; cancer; mineral metabolism disorder;
lipid metabolism disorder; rat; YY-1; splice variant; acceptor site; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H.influenzae detection probe binds to 16S rRNA gene at pos. 1255-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; Haemophilus influenzae; 16S rRNA gene; E.coli; helper probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 62; 193pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT10984 standard; DNA; 14 BP
                                                                                                                                                                                                19-DEC-2003; 2003WO-EP014762.
                                                                                                                                                                                                                                     20-DEC-2002; 2002DE-01061650
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(first entry)
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                                                                                                                                                                                                                                                                                                       Kloeting I, Kloeting N;
                                                                                                                                                                                                                                                                    (UYGR ) UNIV GREIFSWALD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor.
                                                                                                                                                                                                                                                                                                                                          WPI; 2004-507695/48.
                                                                                          Rattus norvegicus
                                                                                                                           WO2004056857-A2
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19-JUN-1996
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Probes AAT10983-4 are used for the specific detection of Haemophilus influenzae. They bind to a region of the H.influenzae 16S rRNA gene at pos. corresp. to bases 837-854 or 1255-69 of the B.coli 16S rRNA gene. The probes can also be used in the detection by the helper probes AAT10985-9. The probes are pref. labelled with an acridinium ester label. The probes are specific for H.influenzae and do not bind to nucleic acids from H.aphrophilus, H.ducrei, H.haemolyticus, H.parahaemolyticus, H.parahluenzae or H.paraphrophilus. (Updated on 25-MAR-2003 to correct Pfield.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
acridinium ester label; H.aphrophilus; H.ducrei; H.haemolyticus;
H.parahaemolyticus; H.parainfluenzae; H.paraphrophilus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of Haemophilus influenzae nucleic acid - using new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%; Score 10; DB 1; Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human EGF-R target sequence nucleotide position 3489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Col 9; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV99057 standard; RNA; 14 BP
                                                                                                                                                                                                                                                                     94US-00221968.
                                                                                                                                                                                                                                                                                                                                91US-00690788.
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97US-00985162.
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(UYAS-) UNIV ASTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
Les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligo:nucleotide probes.
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                                                                                                                                                                                                                                                                                                                                                                                          (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-029808/03.
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                                                                                                                                                                                                                                                                                                                                25-APR-1991;
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04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Milliman CL;
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                                                                                                          The present invention describes enzymatic nucleic acid molecules (NAMS) which specifically cleave RNA derived from an epidermal growth factor receptor (EGP-N) gene. AAV97221 to AAV96043 and AAV9892 to AAV980900 represent specifically claimed target sequence from human EGP-R. AAV98044 to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and hairpin ribozymes respectively for human EGP-R. The NAMS are useful for cleaving EGP-R RNA in the treatment of a condition associated with EGFR expression levels e.g. to inhibit cell proliferation in the prevention or treatment of cancers. The NAMS can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of EGP-R RNA in a cell
                                            Enzymatic nucleic acids - which cleave RNA derived from an epidermal growth factor receptor, useful for inhibiting cell proliferation and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid hybridisation probe specific for Haemophilus influenzae - useful for identification of H. influenzae, optionally used with helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus influenzae; 16S rRNA; probe; hybridisation; identification;
bacterial colony; ribosomal RNA; ss.
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                        13.0%; Score 10; DB 1; Length 14; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                     Sequence 14 BP; 0 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae 16S rRNA probe #1.
Mcswiggen JA;
                                                                                         Claim 6; Page 89; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                       AAV67150 standard; DNA; 14 BP.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENP-) GEN-PROBE INC
                     WPI; 1998-437449/37.
                                                                                                                                                                                                                                                                                                                        49 AGAGCCAGCG
                                                                                                                                                                                                                                                                                                                                            AGAGCCAGCG
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Pell P,
                                                                     treating cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-1999
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01-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5830654-A
Akhtar S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes.
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8 셤 The present sequence represents a nucleic acid hybridisation probe that hybridises to Haemophilus influenzae rRNA in a region corresponding to nucleotides 1255-1268 of E. coli 16S rRNA. The probe can be labelled,

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                                                        probe does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
especially with an acridinium ester, and used in an assay for H. influenzae, optionally together one or more helper probes. The probe doe not hybridise to nucleic acids from H. aphrophilus, H. ducreyi, H. haemolyticus, H. parahemolyticus, H. parainfluenzae or H. paraaphrophilus. The probe enables rapid, non-subjective identification of the presence of specific ribosomal RNA sequences that are unique to all serotypes and bio-types of H. influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; anglogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; anglogenic factor; cytostatic; antidiabetic; ophthalmologic; antilnflammatory; antiatrhritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovageular glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aryl hydrocarbon nuclear transport target site SEQ ID NO:891.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.0%; Score 10; DB 1; Lo 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coeshott C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 53; Page 90; 305pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA17665 standard; RNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US006507.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-591315/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 AGCGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9950403-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
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AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an manNa encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as angiofibrome of tuberous sclerosis, portains stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in mammalian cells. Each vector has a first and second consensus sequence (CS). The CS or their homologues are present in known murine autonomously replicating sequences (MAMRS). The first CS is homologues to AAN92945. The inefficient selection system comprises the tk gene and a truncated tk promoter. The vectors also contain a gene coding for a protein and the necessary promoter and terminator sequences for the expression of this gene. The expression vectors provide rapid amplification, allow selection of best clones in a short time, are of universal utility in mammalian cells, and are free of viral origin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression vectors for mammalian cells - with two consensus sequences and inefficient selection system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The inventors claim vectors for the expression of heterologous proteins
                                                                                                                                                                                                                                                                                                               Gaps
and AAA22476 to AAA23262, AAA23343 to
                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine autonomously replicating sequence; consensus sequence;
                                                                                                                                                                                                                                                                           13.0%; Score 10; DB 1; Length 14;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                   integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus sequence for mammalian expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     Sequence 14 BP; 3 A; 5 C; 2 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                          1.6e+02;
                                                                                                                                                                                                                                                                                    100.0%; Pred. no.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
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integrin subunit beta 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN92945 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                                                                                                                                                                                                                   58 GAAGCTGATG 67
                                                                                                                                                                                                                                                                                                                                                                                   GAAGCTGATG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weidle U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1989-078357/11.
                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAN92945;
                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                             Matches
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Score 9.4; DB 1; Length 12; Pred. No. 1.6e+02;

12.2%; 90.9%;

Query Match Best Local Similarity

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The present invention describes a compound (I) comprising 8-50

"C nucleobases which is targeted to a 5' untranslated region (UTR), coding,
"C nucleobases which is targeted to a 5' untranslated region (UTR), coding,
"A 2, group IIA (synovial), where the compound specifically hybridises with
and inhibits the expression of phospholipase A2, group IIA (synovial).

Also described: (1) a composition comprising the compound and a carrier
or diluent; (2) a method of inhibiting the expression of phospholipase
A2, group IIA in cells or tissues; and (3) a method of treating an animal
c having a disease or condition associated with phospholipase A2, group IIA
(synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
antipsoriatic activities, and can be used in vaccines and in gene
therapy. The compound (I) can be used in vaccines and in gene
treating or preventing inflammation, cancer, psoriasis or diabetes. The
present sequence represents a human phospholipase A2 group IIA (synovial)
ö
                                                                                                                                                                                                                                                                               Phospholipase A2 group IIA; synovial; antisense modulation; inflammation; phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory; antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer; psoriasis; diabetes; ss.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compound that hybridizes with and inhibits the expression of Phospholipase A2, group IIA, useful for preparing a composition for treating or preventing inflammation, cancer, psoriasis or diabetes.
ö
                                                                                                                                                                                                                                                 Human phospholipase A2 antisense oligonucleotide SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "2'-0-methoxyethyl (2'-MOE) gapmer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "2'-0-methoxyethyl (2'-MOE) gapmer"
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "phosphorothioate backbone"
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .5
/*tag= b
/mod_base= OTHER
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/mod_base= OTHER
 ö
                                                                                                                                                  ACC46925 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2002; 2002WO-US016135.
                                                                                                                                                                                                                    (first entry)
 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16. .20
                                  34 TCCTCTGAGAG 44
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                                                               11 TCCTCTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-140495/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   modified base
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens,
                                                                                                                                                                                                                    05-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                   ACC46925;
                                                                                                                  RESULT 294
 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the preferred target sequence of an enzymentic nucleic acid, especially a hairpin ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the target these sites and their activities optimised by either varying the rarget the binding arms or by modification to prevent degradation by nucleases. The ribozymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with hepatocellular carcinoma. The ribozymes may be used in combination with therferon to treat HCV infection, other infectious diseases, autoimmune
                                                                                  ö
                                                                                                                                                                                                                                                                                         Bnzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
chimeric phosphorothioate antisense oligonucleotide, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                   Gaps
                                                                                  ö
                                                                                                                                                                                                                                                                 Substrate for hairpin ribozyme which cleaves HCV at nt. 886.
                                                        12.2%; Score 9.4; DB 1; Length 20; 90.9%; Pred. No. 2.4e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.4%; Score 8.8; DB 1; Length 14; ilarity 83.3%; Pred. No. 2.38+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pavco PA, Macejak
                                   Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blatt L, Mcswiggen JA, Roberts B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 94; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0083217P.
98US-0100842P.
99US-00257608.
99US-00274553.
                                                                                                                                                                                            AAZ64698 standard; RNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US009027.
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                                                                                                                                                                                                                                         (first entry)
                                                                                  Conservative
                                                                                                         CCTCTGAGAGG 45
                                                                                                                               CCTCTCAGAGG 18
                                                                                                                                                                                                                                                                                                       cirrhosis; liver failum
autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-062023/05.
                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1998;
25-FEB-1999;
23-MAR-1999;
                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                 W09955847-A2
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                                                                                                                                                                                                                                           28-MAR-2000
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                                                        Query Match
Best Local S
                                                                                                         35
                                                                                                                                                                                                                   AAZ64698;
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                                                                                                                                                                            Matches
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The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV cribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or replication of hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more coher drug therapies, particularly type I interferon. The present sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection; HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide; liver failure; hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hairpin ribozyme; HP ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus substrate #20 for HCV hairpin ribozyme #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macejack D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8.8; DB 1; Length 14;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roberts B, Pavco PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segdata.uspto.gov/psipsDIDEntry.html
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83.3%;
                                                                                                                                                                                                                           ABX01535 standard, RNA; 14
                                                                                                                                                                                                                                                                                                                                                     23-DEC-2002 (first entry)
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2 AAACAAGACGGC 13
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                                     BLATT L.
MCSWIGGEN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-617759/66.
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PAVCO P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MACEJACK D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS2002082225-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-1999;
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                                                                                                                                                                                                                                                                                            ABX01535;
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                                                                                                                                                                                      ABX01535/c
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Best Local Similarity Matches 10; Conserv

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The invention relates to an enzymatic nucleic acid molecule which specifically cleaves minus strand RNA derived from hepatitis C virus (HCV). The binding arms of the molecule comprise ribozyme sequences. The molecule is selected from inozyme, G-cleaver, DNAzyme, Amberzyme, and Zinzyme motifs. Also described: (1) a pharmaceutical composition comprising the novel enzymatic nucleic acid; (2) a mammalian cell including the novel enzymatic nucleic acid; (3) an expression vector comprising a nucleic acid sequence encoding at least one enzymatic nucleic acid molecule, (4) a mammalian cell including at least one enzymatic molecule, (4) a mammalian cell including an expression vector of (3); (5) methods for treating to a patient the novel enzymatic nucleic acid or the vector of (3); (6) a method of treating a patient having a condition associated with HCV infection, by contacting cells of the patient with the respicated with HCV infection, by contacting cells of the patient with the respectate RNA molecule, py contacting the novel enzymatic nucleic acid or the novel enzymatic nucleic acid and cell or inhibiting the expression of HCV minus strand. The nucleic acid may also be used to treat or prevent the occurrence of a disease state in a patient. The present sequence represents an HCV nucleic acid may also be used to treat or prevent the occurrence of a disease state in a patient. The present sequence represents an HCV nucleic acid may also be used to treat or prevent the occurrence of a disease state in a patient. The presents sequence represents an HCV nucleic acid and the patient is used in the
                                                                                                                                                                                                                                                                      ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection; antiviral; gene therapy; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New enzymatic nucleic acid molecule, which specifically cleaves minus strand RNA derived from hepatitis C virus, useful for modulating the expression and/or replication of hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8.8; DB 1; Length 14; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macejack D;
                                                                                                                                                                                                                                       Hepatitis C virus hairpin ribozyme substrate sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pavo PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 43; 65pp; English.
                                                                                                                     AEB76459 standard; RNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-FEB-2000; 2000US-00504231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00274553.
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14 AAACAGGACAGC 3
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MCSWIGGEN J A.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-215899/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of
                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                              US2002013458-A1.
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(MCSW/)
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AEB76459/c
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The invention relates to a kit for detecting aquatic animal pathogens and human pathogens, comprising a pair of PCR primers used to detect specific DNA fragments of Vibrio fluvialis. The kit and method can be used in bacteria tracking and detection of aquatic animal pathogens in the course of breeding and also in the clinical detection of human intestinal acute infections, as well as in environmental monitoring. This sequence represents a PCR primer used in the scope of the invention.
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kit for diagnosing gene of pathogenic bacterial and river vibrion of aquatic animal and human and testing method thereof.
                                                                                                                                                                                                                                             Microorganism detection, PCR, primer, intestine infection, gastrointestinal-gen., gastrointestinal disease, infection; ss.
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ALDOB gene allele-specific primer SEQ ID NO: 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ALDOB; fructose-bisphosphate aldolase B; SNP; single nucleotide polymorphism; primer; probe; ss.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYZH-) UNIV ZHONGSHAN
                                                       14 AAACAGGACAGC
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                                                                                                                                                                                                                                                                                        Vibrio fluvialis.
                                                                                                                                                                                                                  PCR primer #1
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Matches
 Matches
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Query Match Best Local Similarity

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Homo sapiens.

WACO03091454-A1.

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Query Match 10.9%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 1.9e+02; Matches 9; Conservative 0; Mismatches 1; Indels

Search completed: April 19, 2006, 16:12:08 Job time : 0.001 secs .

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